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<p>(21) International Application Number: PCT/US00/06707</p> <p>(22) International Filing Date: 09 May 2000 (09.05.2000)</p> <p>(30) Priority Data: 60/133,423 11 May 1999 (11.05.1999) US</p> <p>(60) Parent Application or Grant ELI LILLY AND COMPANY [/]; O. BECKER, Gerald, Wayne [/]; O. HALE, John, Edward [/]; O. HEATH, William, Francis, Jr. [/]; O. JOHNSTONE, Edward, Marion [/]; O. LITTLE, Sheila, Parks [/]; O. TU, Yuan [/]; O. YEH, Wu- Kuang [/]; O. YIN, Tinggui [/]; O. BECKER, Gerald, Wayne [/]; O. HALE, John, Edward [/]; O. HEATH, William, Francis, Jr. [/]; O. JOHNSTONE, Edward, Marion [/]; O. LITTLE, Sheila, Parks [/]; O. TU, Yuan [/]; O. YEH, Wu-Kuang [/]; O. YIN, Tinggui [/]; O. WILSON, Alexander; O.</p>		
<p>(54) Title: AMYLOID PRECURSOR PROTEIN PROTEASE AND RELATED NUCLEIC ACID COMPOUNDS (54) Titre: PROTEASE DE PROTEINE PRECURSEUR AMYLOÏDE ET COMPOSÉS D'ACIDES NUCLÉIQUES APPARENTÉS</p> <p>(57) Abstract This present invention provides an amyloid precursor protein protease and related nucleic acid compounds thereof. The invention also provides compositions, expression vectors, and transfected host cells as well as assays and methods of use. The compounds of the present invention will further characterize Alzheimer's Disease and other neurodegenerative disease states.</p> <p>(57) Abrégé La présente invention concerne une protéase de protéine précurseur amyloïde et des composés d'acides nucléiques apparentés. Cette invention concerne aussi des compositions, des vecteurs d'expression, des cellules hôtes transfectées, de même que des dosages et des techniques d'utilisation. Les composés de cette invention permettront de mieux cerner la maladie d'Alzheimer et d'autres états liés à une maladie neurodégénérative.</p>		

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(21) International Application Number: PCT/US00/06707	(74) Agents: WILSON, Alexander et al.; Eli Lilly and Company, Lilly Corporate Center, Indianapolis, IN 46285 (US).	
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(71) Applicant (<i>for all designated States except US</i>): ELI LILLY AND COMPANY (US/US); Lilly Corporate Center, Indianapolis, IN 46285 (US).		
(72) Inventors; and	Published	
(75) Inventors/Applicants (<i>for US only</i>): BECKER, Gerald, Wayne (US/US); 10815 East 121st Street, Fishers, IN 46038 (US). HALE, John, Edward (US/US); 2644 Forest Drive, Fishers, IN 46038 (US). HEATH, William, Francis, Jr. (US/US); 11214 Tufton Street, Fishers, IN 46038 (US). JOHNSTONE, Edward, Marion (US/US); 5129 East 69th Street, Indianapolis, IN 46220 (US). LITTLE, Sheila, Parks (US/US); 4480 North Meridian Street, Indianapolis, IN 46208 (US). TU, Yuan (US/US); 10848 Madeline Court, Fishers, IN 46038 (US). YEII, Wu-Kuang (US/US); 720 Primrose Court, Greenwood, IN 46142 (US). YDN, Tinggui (CN/US); 409 Mari Way, Carmel, IN 46032 (US).		
(54) Title: AMYLOID PRECURSOR PROTEIN PROTEASE AND RELATED NUCLEIC ACID COMPOUNDS		
(57) Abstract		
<p>This present invention provides an amyloid precursor protein protease and related nucleic acid compounds thereof. The invention also provides compositions, expression vectors, and transfected host cells as well as assays and methods of use. The compounds of the present invention will further characterize Alzheimer's Disease and other neurodegenerative disease states.</p>		

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Description

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**AMYLOID PRECURSOR PROTEIN PROTEASE AND RELATED
NUCLEIC ACID COMPOUNDS**

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5 This invention relates to proteases which cleave amyloid precursor protein and facilitate β -amyloid peptide release, and accordingly, have utility in identifying compounds which treat or prevent Alzheimer's Disease.

20

Alzheimer's disease is a degenerative brain disorder
10 characterized clinically by progressive loss of memory, cognition, reasoning, judgment, and emotional stability that gradually leads to profound mental deterioration and ultimately death. Alzheimer's disease is a very common cause of progressive mental failure (dementia) in aged humans and is believed to represent the fourth most common medical cause of death in the
25 United States. Alzheimer's disease has been observed in races and ethnic groups worldwide and presents a major present and future public health problem. The disease is currently estimated to affect about two to three million individuals in the United States alone. Alzheimer's disease is at present incurable. No treatment that effectively prevents Alzheimer's disease
30 or reverses its symptoms and course is currently known.

35

The brains of individuals with Alzheimer's disease exhibit characteristic lesions termed senile (or amyloid) plaques, amyloid angiopathy (amyloid deposits in blood vessels) and neurofibrillary tangles. Large numbers of these lesions, particularly amyloid plaques and neurofibrillary
40 25 tangles, are generally found in several areas of the human brain important for memory and cognitive function in patients with Alzheimer's disease.
45 Smaller numbers of these lesions in a more restrictive anatomical distribution are also found in the brains of most aged humans who do not have clinical Alzheimer's disease. Amyloid plaques and amyloid angiopathy
50 30 also characterize the brains of individuals with Trisomy 21 (Down's

55

syndrome) and Hereditary Cerebral Hemorrhage with Amyloidosis of the Dutch-Type (HCHWA-D).

10

The principal chemical constituent of the amyloid plaques and vascular amyloid deposits (amyloid angiopathy), characteristic of Alzheimer's disease and the other disorders mentioned above, is an approximately 4.2 kilodalton (kD) protein of about 39-43 amino acids designated the β -amyloid peptide (this protein is also referred to in the literature as β AP, A β , A β P, A-beta, or β /A4). β -Amyloid peptide was first purified and a partial amino acid sequence was provided by Glenner, et al., Biochemical and Biophysical Research Communications, 120:885-890 (1984). The isolation procedure and the sequence data for the first 28 amino acids are described in United States Patent 4,666,829, the entire contents of which are herein incorporated by reference.

15

Several lines of evidence indicate that progressive cerebral deposition of β -amyloid peptide plays a seminal role in the pathogenesis of Alzheimer's disease and can precede cognitive symptoms by years or decades. See, e.g., D. Selkoe, Neuron, 6:487-498 (1991). An important line of evidence is the discovery that missense DNA mutations at amino acid 717 of the 770-amino acid isoform of amyloid precursor protein can be found in affected members, but not unaffected members, of several families with a genetically determined (familial) form of Alzheimer's disease. Goate, et al., Nature (London), 349:704-706 (1990). Genetic linkage studies have demonstrated that this mutation, as well as certain other mutations in the amyloid precursor protein gene, are the specific molecular cause of Alzheimer's disease in the affected members of such families. In addition, a mutation at amino acid 693 of the 770-amino acid isoform of amyloid precursor protein has been identified as the cause of the β -amyloid peptide deposition disease, and a change from alanine to glycine at amino acid 692 appears to cause a phenotype that resembles Alzheimer's disease in some patients. The discovery of these and other mutations in amyloid precursor protein in

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- 3 -

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genetically based cases of Alzheimer's disease support the hypothesis that alteration of amyloid precursor protein and subsequent deposition of its β -amyloid peptide fragment can cause Alzheimer's disease.

15

Molecular biological and protein chemical analyses have shown
5 that the β -amyloid peptide is a small fragment of a much larger precursor
protein, the amyloid precursor protein (APP), that is normally produced by
cells in many tissues of various animals, including humans. Knowledge of the
structure of the gene encoding the amyloid precursor protein has
demonstrated that the β -amyloid peptide arises as a peptide fragment that is
20 cleaved from the amyloid precursor protein by proteases.

20

It is presently believed that a normal (i.e., non-pathogenic)
25 processing of the amyloid precursor protein occurs via cleavage by a putative
" α -secretase" which cleaves between amino acids 16 and 17 of the β -amyloid
peptide region within the protein. Kang, et al., *Nature (London)*, 325:773-776
15 (1987). It is further believed that pathogenic processing occurs in part via an
enzyme designated " β -secretase" which cleaves at the amino-terminus of the
30 β -amyloid peptide region within the precursor protein.

30

The identification, isolation, and purification of the proteases
35 involved in the processing of amyloid precursor protein would permit
20 chemical modeling of a critical event in the pathology of Alzheimer's disease
and would allow the screening of compounds to determine their ability to
inhibit formation of β -amyloid peptide.

40

Despite the progress which has been made in understanding the
underlying mechanisms of Alzheimer's disease and other β -amyloid peptide-
25 related diseases, there remains a need to develop methods and compositions
for treatment of the diseases. Ideally, the treatment methods would
45 advantageously be based on drugs which are capable of inhibiting β -amyloid
peptide release and/or its synthesis in vivo.

50

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- 4 -

10 The present invention provides an isolated protein useful as an
amyloid precursor protein protease, said compound comprising the amino acid
sequence

Met Leu Arg Arg Arg Gly Ser Pro Gly
5 1 5

15 Met Gly Val His Val Gly Ala Ala Leu Gly Ala Leu Trp Phe Cys Leu
10 15 20 25

20 Thr Gly Ala Leu Glu Val Gln Val Pro Glu Asp Pro Val Val Ala Leu
20 30 35 40

25 Val Gly Thr Asp Ala Thr Leu Cys Cys Ser Phe Ser Pro Glu Pro Gly
25 45 50 55

30 Phe Ser Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys
30 60 65 70

35 Gln Leu Val His Ser Phe Ala Glu Gly Gln Asp Gln Gly Ser Ala Tyr
35 75 80 85

40 Ala Asn Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala
40 90 95 100 105

45 Ser Leu Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly Ser Phe Thr
45 110 115 120

50 Cys Phe Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val Ser Leu Gln
50 125 130 135

55 Val Ala Ala Pro Tyr Ser Lys Pro Ser Met Thr Leu Glu Pro Asn Lys
55 140 145 150

60 Asp Leu Arg Pro Gly Asp Thr Val Thr Ile Thr Cys Ser Ser Tyr Gln
60 155 160 165

55

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- 5 -

Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln Asp Gly Gln Gly Val Pro
170 175 180 185

10

Leu Thr Gly Asn Val Thr Thr Ser Gln Met Ala Asn Glu Gln Gly Leu
5 190 195 200

15

Phe Asp Val His Ser Ile Leu Arg Val Val Leu Gly Ala Asn Gly Thr
205 210 215

20

10 Tyr Ser Cys Leu Val Arg Asn Pro Val Leu Gln Gln Asp Ala His Ser
220 225 230

25

Ser Val Thr Ile Thr Pro Gln Arg Ser Pro Thr Gly Ala Val Glu Val
235 240 245

30

Gln Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr
250 255 260 265

35

Leu Arg Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu
20 270 275 280

40

Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe
285 290 295

45

25 Thr Glu Gly Arg Asp Gln Gln Ser Ala Tyr Ala Asn Arg Thr Ala Leu
300 305 310

50

40 Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg
315 320 325

55

30 Val Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg
330 335 340 345

45 Asp Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala Pro Tyr Ser
35 350 355 360

5

- 6 -

Lys Pro Ser Met Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp
365 370 375

10

Thr Val Thr Ile Thr Cys Ser Ser Tyr Arg Gly Tyr Pro Glu Ala Glu
5 380 385 390

15

Val Phe Trp Gln Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr
395 400 405

20

10 Thr Ser Gln Met Ala Asn Glu Gln Gly Leu Phe Xaa Xaa Xaa Xaa Xaa
410 415 420 425

Xaa
430 435 440

25

15 Xaa Xaa Xaa Xaa Xaa Asp Ala His Gly Ser Val Thr Ile Thr Gly
445 450 455

30

Gln Pro Met Thr Phe Pro Pro Glu Ala Leu Trp Val Thr Val Gly Leu
20 460 465 470

35

Ser Val Cys Leu Ile Ala Leu Leu Val Ala Leu Ala Phe Val Cys Trp
475 480 485

40

25 Arg Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala Gly Ala Glu Asp
490 495 500 505

Gln Asp Gly Glu Gly Glu Ser Lys Thr Ala Leu Gln Pro Leu Lys
510 515 520

30 His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile Ala
525 530 535

hereinafter referred to as SEQ ID NO:2.

More preferred is the amyloid precursor protein protease
35 comprising the amino acid sequence

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- 7 -

Met Leu Arg Arg Arg Gly Ser Pro Gly
1 5

10

Met Gly Val His Val Gly Ala Ala Leu Gly Ala Leu Trp Phe Cys Leu
5 10 15 20 25

15

Thr Gly Ala Leu Glu Val Gln Val Pro Glu Asp Pro Val Val Ala Leu
30 35 40

20

10 Val Gly Thr Asp Ala Thr Leu Cys Cys Ser Phe Ser Pro Glu Pro Gly
45 50 55

25

Phe Ser Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys
60 65 70

15

Gln Leu Val His Ser Phe Ala Glu Gly Gln Asp Gln Gly Ser Ala Tyr
75 80 85

30

Ala Asn Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala
20 90 95 100 105

35

Ser Leu Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly Ser Phe Thr
110 115 120

25

Cys Phe Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val Ser Leu Gln
125 130 135

40

Val Ala Ala Pro Tyr Ser Lys Pro Ser Met Thr Leu Glu Pro Asn Lys
140 145 150

30

Asp Leu Arg Pro Gly Asp Thr Val Thr Ile Thr Cys Ser Ser Tyr Gln
155 160 165

50

35 Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln Asp Gly Gln Gly Val Pro
170 175 180 185

55

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- 8 -

10	Leu Thr Gly Asn Val Thr Thr Ser Gln Met Ala Asn Glu Gln Gly Leu		
	190	195	200
5	Phe Asp Val His Ser Ile Leu Arg Val Val Leu Gly Ala Asn Gly Thr		
	205	210	215
15	Tyr Ser Cys Leu Val Arg Asn Pro Val Leu Gln Gln Asp Ala His Ser		
	220	225	230
20	Ser Val Thr Ile Thr Pro Gln Arg Ser Pro Thr Gly Ala Val Glu Val		
	235	240	245
25	Gln Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr		
	250	255	260
	265		
30	Leu Arg Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu		
	270	275	280
20	Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe		
	285	290	295
35	Thr Glu Gly Arg Asp Gln Gly Ser Ala Tyr Ala Asn Arg Thr Ala Leu		
	300	305	310
25			
40	Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg		
	315	320	325
30	Val Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg		
	330	335	340
45			
35	Asp Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser		
	350	355	360
50	Lys Pro Ser Met Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp		

55

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- 10 -

antisense mRNA are also provided. A particularly preferred nucleic acid compound is the DNA compound comprising the sequence

10

5 atgtgtcagc cgcctcacag gaag atg ctg cgt cgg cgg ggc agc cct ggc 51
Met Leu Arg Arg Arg Gly Ser Pro Gly
1 5

15

10 atg ggt gtg cat gtg ggt gca gcc ctg gga gca ctg tgg ttc tgc ctc 99
Met Gly Val His Val Gly Ala Ala Leu Gly Ala Leu Trp Phe Cys Leu
10 10 15 20 25

20

20 aca gga gcc ctg gag gtc cag gtc cct gaa gac cca gtg gtg gca ctg 147
Thr Gly Ala Leu Glu Val Val Gln Val Pro Glu Asp Pro Val Val Ala Leu
30 35 40

25

15 gtg ggc acc gat gcc acc ctg tgc tgc tcc tcc cct gag cct ggc 195
Val Gly Thr Asp Ala Thr Leu Cys Cys Ser Phe Ser Pro Glu Pro Gly
45 50 55

30

20 ttc agc ctg gca cag ctc aac ctc atc tgg cag ctg aca gat acc aaa 243
Phe Ser Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys
60 65 70

35

25 cag ctg gtg cac agc ttt gct gag ggc cag gac cag ggc agc gcc tat 291
Gln Leu Val His Ser Phe Ala Glu Gly Gln Asp Gln Gly Ser Ala Tyr
75 80 85

40

30 gcc aac cgc acg gcc ctc ttc ccg gac ctg ctg gca cag ggc aac gca 339
Ala Asn Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala
90 95 100 105

45

tcc ctg egg ctg cag cgc gtg cgt gtg gcg gac gag ggc agc aac acc 387
Ser Leu Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly Ser Phe Thr
110 115 120

50

35 tgc ttc gtg agc atc cgg gat ttc ggc agc gct gcc gtc agc ctg cag 435

55

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- 11 -

Cys Phe Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val Ser Leu Gln
 125 130 135

10

5 140 145 150
 stg gcc gct ccc tac tcg aag ccc agc atg acc ctg gag ccc aac aag 483
 val Ala Ala Pro Tyr Ser Lys Pro Ser Met Thr Leu Glu Pro Asn Lys

15

10 155 160 165
 gac ctg cgg cca ggg gac acg gtg acc atc acg tgc tcc agc tec cag 531
 Asp Leu Arg Pro Gly Asp Thr Val Thr Ile Thr Cys Ser Ser Tyr Gln

20

170 175 180 185
 ggc tac cct gag gct gag gtg ttc tgg cag gat ggg cag ggt gtg ccc 579
 Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln Asp Gly Gln Gly Val Pro

25

15 190 195 200
 ctg act ggc aac gtg acc acg tcg cag atg gcc aac gag cag ggc ttg 627
 Leu Thr Gly Asn Val Thr Ser Gln Met Ala Asn Glu Gln Gly Leu

30

20 205 210 215
 ttt gat gtg cac agc att ctg cgg gtg ctg ggt gca aat ggc acc 675
 Phe Asp Val His Ser Ile Leu Arg Val Val Leu Gly Ala Asn Gly Thr

35

25 220 225 230
 tac agc tgc ttg gtg cgc aac ccc gtc ctg cag cag gat ggc cac agc 723
 Tyr Ser Cys Leu Val Arg Asn Pro Val Leu Gln Gln Asp Ala His Ser

40

30 235 240 245
 tct gtc acc atc aca ccc cag aga agc ccc aca gga gcc gtg gag gtc 771
 Ser Val Thr Ile Thr Pro Gln Arg Ser Pro Thr Gly Ala Val Glu Val

45

250 255 260 265
 cag gtc cct gag gac ccg gtg gtc gcc cta gtg ggc acc gat gcc acc 819
 Gln Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr

50

35 270 275 280
 ctg cgc tgc tcc ttc tcc ccc gag cst ggc ttc agc ctg gca cag ctc 867

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- 12 -

Leu Arg Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu
270 275 280

10

aac ctc atc tgg cag ctg aca gac acc aac cag ctg gtg cac agt ttc 915
5 Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe
285 290 295

15

acc gaa ggc cgg gac cag ggc agc gcc tat gcc aac cgc acg gcc ctc 963
Thr Glu Gly Arg Asp Gln Gly Ser Ala Tyr Ala Asn Arg Thr Ala Leu
10 300 305 310

20

tcc ccg gac ctg ctg gca caa ggc aat gca tcc ctg agg ctg cag cgc 1011
Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg
315 320 325

15

gtg cgt gtg gcg gac gag ggc agc ttc acc tgc ttc gtg agc atc cgg 1059
Val Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg
330 335 340 345

30

20 gat ttc ggc agc gct gcc gtc agc ctg cag gtg gcc gct ccc tac tcc 1107
Asp Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser
350 355 360

35

aag ccc agc atg acc ctg gag ccc aac aag gac ctg cgg cca ggg gac 1155
25 Lys Pro Ser Met Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp
365 370 375

40

acg gtg acc atc acg tgc tcc agc tac cgg ggc tac cct gag gct gag 1203
Thr Val Thr Ile Thr Cys Ser Ser Tyr Arg Gly Tyr Pro Glu Ala Glu
30 380 385 390

45

gtg ttc tgg cag gat ggg cag ggt gtg ccc ctg act ggc aac gtg acc 1251
Val Phe Trp Gln Asp Cys Gln Gly Val Pro Leu Thr Gly Asn Val Thr
395 400 405

35

acg tcg cag atg gcc aac gag cag ggc ttg ttt nnn nnn nnn nnn nnn 1299

55

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- 13 -

Thr Ser Gln Met Ala Asn Glu Gln Gly Leu Phe Xaa Xaa Xaa Xaa Xaa

410 415 420 425

10

nnn 1347

5 Xaa Xaa

430 435 440

15

nnn nnn nnn nnn nnn gat gcg cac ggc tct gtc acc atc aca ggg 1395
Xaa Xaa Xaa Xaa Xaa Xaa Asp Ala His Gly Ser Val Thr Ile Thr Gly

10 445 450 455

20

cag cct atg aca ttc ccc cca gag gcc ctg tgg gtg ecc gtg ggg ctg 1443
Gln Pro Met Thr Phe Pro Pro Glu Ala Leu Trp Val Thr Val Gly Leu

460 465 470

25

tct gtc tgt ctc att gca ctg ctg gtg gcc ctg gct ttc gtg tgc tgg 1491
Ser Val Cys Leu Ile Ala Leu Leu Val Ala Leu Ala Phe Val Cys Trp

475 480 485

30

20 aga aag atc aaa cag agc tgt gag gag gag aat gca gga gct gag gac 1539
Arg Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala Gly Ala Glu Asp

490 495 500 505

35

25 cag gat ggg gag gga gaa ggc tcc aag aca gcc ctg cag cct ctg aas 1587
Gln Asp Gly Glu Gly Glu Gly Ser Lys Thr Ala Leu Gln Pro Leu Lys

510 515 520

40

cac tct gac agc aca gaa gat gat gga caa gaa ata gcc tga 1629
His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile Ala

30 525 530 535

45

ccatgaggac cagggagctg ctacccctcc ctacagctcc taccctctgg ctgc 1683

hereinafter referred to as SEQ ID NO:1.

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35 However, an even more preferred isolated nucleic acid compound
is the DNA compound having the sequence

55

5

- 15 -

	gtg gcc gct ccc tac tgg aag ccc agc atg acc ctg gag ccc sac aag	483		
10	Val Ala Ala Pro Tyr Ser Lys Pro Ser Met Thr Leu Glu Pro Asn Lys			
	140	145	150	
5				
	gac ctg cgg cca ggg gac acg gtg acc atc acg tgc tcc agc tac cag	531		
15	Asp Leu Arg Pro Gly Asp Thr Val Thr Ile Thr Cys Ser Ser Tyr Gln			
	155	160	165	
10	ggc tac cct gag gct gag gtg ttc tgg cag gat ggg cag ggt gtg ccc	579		
20	Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln Asp Gly Gln Gly Val Pro			
	170	175	180	185
15	ctg act ggc aac gtg acc acg tgg cag atg ggc sac gag cag ggc ttg	627		
25	Leu Thr Gly Asn Val Thr Ser Gln Met Ala Asn Glu Gln Gly Leu			
	190	195	200	
20	ttt gat gtg cac agc atc ctg cgg gtg ctg ggt gca aat ggc acc	675		
30	Phe Asp Val His Ser Ile Leu Arg Val Val Leu Gly Ala Asn Gly Thr			
	205	210	215	
35	tac agc tgc ctg gtg cgc sac ccc gtg ctg cag gat gcg cac agc	723		
	Tyr Ser Cys Leu Val Arg Asn Pro Val Leu Gln Gln Asp Ala His Ser			
	220	225	230	
25				
	tct gtc acc atc aca ccc cag aga agc ccc aca gga gcc gtg gag gtc	771		
40	Ser Val Thr Ile Thr Pro Gln Arg Ser Pro Thr Gly Ala Val Glu Val			
	235	240	245	
30	cag gtc cct gag gac ccg gtg gcc cta gtg ggc acc gat gcc acc	819		
45	Gln Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr			
	250	255	260	265
35	ctg cgc tgc tcc ttc tcc ccc gag cct ggc ttc agc ctg gca cag ctc	867		
50	Leu Arg Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu			
	270	275	280	

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	aac ctc atc tgg cag ctg aca gac acc aaa cag ctg gtg cac agt ttc	915		
10	Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe			
	285	290	295	
5	acc gaa ggc cgg gac cag ggc agc gcc tat gcc aac cgc acg gcc ctc	963		
15	Thr Glu Gly Arg Asp Gln Gly Ser Ala Tyr Ala Asn Arg Thr Ala Leu			
	300	305	310	
10	tcc ccg gac ctg ctg gca caa ggc aat gca tcc ctg agg ctg cag cgc	1011		
20	Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg			
	315	320	325	
25	gtg cgt gtg gcg gac gag ggc agc ttc acc tgc ttc gtg agc atc cgg	1059		
15	Val Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg			
	330	335	340	345
30	gat ttc ggc agc gct gcc gtc agc ctg cag gtg gcc gct ccc tac tcc	1107		
20	Asp Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser			
	350	355	360	
35	aag ccc agc atg acc ctg gag ccc aac aag gac ctg cgg cca ggg gac	1155		
	Lys Pro Ser Met Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp			
	365	370	375	
25	acg gtg acc atc acg tgc tcc agc tac cgg ggc tac cct gag gct gag	1203		
	Thr Val Thr Ile Thr Cys Ser Ser Tyr Arg Gly Tyr Pro Glu Ala Glu			
40	380	385	390	
30	gtg ttc tgg cag gat ggg cag ggt gtg ccc ctg act ggc aac gtg acc	1251		
45	Val Phe Trp Gln Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr			
	395	400	405	
35	acg tcg cag atg gcc aac gag cag ggc ttg ttg gat gtg cac agc gtc	1299		
	Thr Ser Gln Met Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Val			
50	410	415	420	425

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	ctg cgg gtg gtc ctg ggt gcg aat ggc acc tac agc tgc ctg gtg cgc	1347		
10	Leu Arg Val Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg			
	430	435	440	
	5			
	aac ccc gtg ctg cag cag gat gcg cac ggc tct gtc acc atc aca ggg	1395		
15	Asn Pro Val Leu Gln Gln Asp Ala His Gly Ser Val Thr Ile Thr Gly			
	445	450	455	
	10 cag cct atg aca ttc ccc cca gag gcc ctg tgg gtg acc gtg ggg ctg	1443		
20	Gln Pro Met Thr Phe Pro Pro Glu Ala Leu Trp Val Thr Val Gly Leu			
	460	465	470	
	25 tct gtc tgt ctc att gca ctg ctg gtg gcc ctg gct ttc gtg tgc tgg	1491		
	Ser Val Cys Leu Ile Ala Leu Leu Val Ala Leu Ala Phe Val Cys Trp			
	475	480	485	
	30 aga aag atc aaa cag agc tgt gag gag aat gca gga gct gag gac	1539		
	Arg Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala Gly Ala Glu Asp			
	490	495	500	505
	35 cag gat ggg gag gga gaa ggc tcc aag aca gcc ctg cag cct ctg aaa	1587		
	Gln Asp Gly Glu Gly Glu Ser Lys Thr Ala Leu Gln Pro Leu Lys			
	510	515	520	
	25 cac tct gac agc aaa gaa gat gat gga caa gaa ata gcc tga	1629		
	His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile Ala			
	525	530	535	
	30 ccatgaggac cagggagctg ctacccctcc ctacagctcc taccctctgg ctgc	1683		

45

hereinafter referred to as SEQ ID NO:3.

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Also provided by the present invention are nucleic acid vectors comprising nucleic acids which encode SEQ ID NO:2 or SEQ ID NO:4 or 35 functional equivalents thereof. The preferred nucleic acid vectors are those which are DNA. Most preferred are DNA vectors which comprise the DNA

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sequence which is SEQ ID NO:3. Moreover, DNA vectors of the present invention preferably comprise a promoter positioned to drive expression of said DNA sequence. Those vectors wherein said promoter functions in human embryonic kidney cells (293 cells), AV12 cells, yeast cells or *E.coli* cells are preferred.

15

20

The present invention also provides probes and primers useful for molecular biology techniques. A compound which encodes all or part of SEQ ID NO:2 or SEQ ID NO:4 and which is at least 18 consecutive base pairs in length is provided. Preferably, the 18 base pair or more compound is DNA. Most preferred for this use are the DNA compounds which comprise at least 18 consecutive base pairs of SEQ ID NO:1 or SEQ ID NO:3.

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30

Host cells which harbor the nucleic acids provided by the present invention are also provided. A preferred host cell is an oocyte. A preferred oocyte is one which has been injected with sense mRNA or DNA compounds of the present invention. A more preferred oocyte is one which has been injected with sense mRNA or DNA compounds of the present invention in conjunction with DNA or sense mRNA which encodes APP.

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Further, this invention provides cells into which the nucleic acid compounds of the present invention may be transfected. Host cells include those which are transfected with a nucleic acid compound which encodes SEQ ID NO:2 or SEQ ID NO:4. Preferred cells include host cells transfected with a DNA vector comprising SEQ ID NO:1 or SEQ ID NO:3. The preferred transfected host cells which encode SEQ ID NO:2 or SEQ ID NO:4 are 293 cells, AV12 cells, yeast cells and *E. coli* cells. Also preferred is a host cell which has been co-transfected with a DNA vector which comprises SEQ ID NO:1 or SEQ ID NO:3 and a DNA vector which comprises the coding sequence of APP. 293 cells, AV12 cells, yeast cells and *E. coli* cells are the preferred co-transfected host cells.

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Additionally, the invention provides a method for identifying DNA homologous to a probe of the present invention, which comprises combining test

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- 19 -

nucleic acid with the probe under hybridizing conditions and identifying those test nucleic acids which hybridize.

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Assays utilizing the compounds provided by the present invention are also provided. The assays provided determine whether a substance is a

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5 ligand for β -secretase, said method comprising contacting β -secretase with said substance, monitoring β -secretase activity by physically detectable means, and identifying those substances which interact with or affect β -secretase. Preferred assays of the present invention include a cell culture assay, a high-performance liquid chromatography (HPLC) assay or a synthetic competition assay. Pre-

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ferred cell culture assays utilize oocytes, AV12, *E. coli*, yeast or 293 cells which co-express nucleic acids which encode β -secretase and APP.

25

The invention also provides methods for constructing a host cell capable of expressing a nucleic acid compound which encodes an amino acid compound comprising SEQ ID NO:2 or SEQ ID NO:4, said methods comprising

15 transfecting a host cell with a DNA vector comprising a nucleic acid compound encoding SEQ ID NO:2 or SEQ ID NO:4. A preferred method utilizes 293, AV12, yeast or *E. coli* cells as the host cells. A more preferred method includes a DNA vector which comprises SEQ ID NO:1 or SEQ ID NO:3. A most preferred method includes a DNA vector which comprises SEQ ID NO:3. Another preferred
30
method comprises (a) a DNA vector which comprises SEQ ID NO:3 and (b) a DNA expression vector which encodes the APP coding sequence.

35

40 Additionally, methods for expressing a nucleic acid sequence which encodes SEQ ID NO:2 or SEQ ID NO:4, or functional equivalents thereof, in a transfected host cell, are also provided. These methods comprise culturing a
25 transfected host cell of the present invention under conditions suitable for gene expression. A preferred method utilizes 293, AV12, yeast or *E. coli* cells as the transfected host cell. A more preferred method utilizes a DNA vector to
45 transfect the host cell. A most preferred method utilizes a DNA vector comprising all or part of SEQ ID NO:3.

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- 20 -

The present invention also provides processes for isolating and purifying an amyloid precursor protein protease, said process comprising: (a) establishing in a suitable medium, a culture of the host cells transformed with a polynucleotide encoding an amyloid precursor protein protease; and (b) isolating said protease from said culture. Compositions comprising a peptide isolated according to such processes are also provided.

10

In addition, polyclonal and monoclonal antibodies to the peptides of the present invention are also provided.

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20 The terms and abbreviations used in this document have their normal meanings unless otherwise designated. For example "°C" refers to degrees Celsius; "N" refers to normal or normality; "mmol" refers to millimole or millimoles; "g" refers to gram or grams; "ml" means milliliter or milliliters; "M" refers to molar or molarity; "μg" refers to microgram or micrograms; "μl" refers to microliter or microliters; "pU" refers to pico Unit, and the like.

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30 All nucleic acid sequences, unless otherwise designated, are written in the direction from the 5' end to the 3' end, frequently referred to as "5' to 3'".

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35 All amino acid or protein sequences, unless otherwise designated, are written commencing with the amino terminus ("N-terminus") and concluding with the carboxy terminus ("C-terminus").

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40 "Base pair" or "bp" as used herein refers to DNA or RNA. The abbreviations A, C, G, and T correspond to the 5'-monophosphate forms of the deoxyribonucleosides (deoxy)adenosine, (deoxy)cytidine, (deoxy)guanosine, 45 and (deoxy)thymidine, respectively, when they occur in DNA molecules. The abbreviations U, C, G, and A correspond to the 5'-monophosphate forms of the ribonucleosides uridine, cytidine, guanosine, and adenosine, respectively when they occur in RNA molecules. In double stranded DNA, base pair may refer to a partnership of A with T or C with G. In a DNA/RNA, heteroduplex

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base pair may refer to a partnership of A with U or C with G. (See the definition of "complementary", *infra*.)

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The terms "digestion" or "restriction" of DNA refers to the catalytic cleavage of the DNA with a restriction enzyme that acts only at certain sequences in the DNA ("sequence-specific endonucleases"). The various restriction enzymes used herein are commercially available and their reaction conditions, cofactors, and other requirements were used as would be known to one of ordinary skill in the art. Appropriate buffers and substrate amounts for particular restriction enzymes are specified by the manufacturer or can be readily found in the literature.

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"Ligation" refers to the process of forming phosphodiester bonds between two double stranded nucleic acid fragments. Unless otherwise provided, ligation may be accomplished using known buffers and conditions with a DNA ligase, such as T4 DNA ligase.

25

15 The term "plasmid" refers to an extrachromosomal (usually) self-replicating genetic element. Plasmids are generally designated by a lower case "p" preceded and/or followed by letters and/or numbers. The starting plasmids herein are either commercially available, publicly available on an unrestricted basis, or can be constructed from available plasmids in accordance with published procedures. In addition, equivalent plasmids to those described are known in the art and will be apparent to the ordinarily skilled artisan.

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20 The term "reading frame" means the nucleotide sequence from which translation occurs "read" in triplets by the translational apparatus of transfer RNA (tRNA) and ribosomes and associated factors, each triplet corresponding to a particular amino acid. To insure against improper translation, the triplet codons corresponding to the desired polypeptide must be aligned in multiples of three from the initiation codon, i.e. the correct "reading frame" being maintained.

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"Recombinant DNA cloning vector" as used herein refers to any autonomously replicating agent, including, but not limited to, plasmids and phages, comprising a DNA molecule to which one or more additional DNA segments can or have been added.

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5 The term "recombinant DNA expression vector" as used herein refers to any recombinant DNA cloning vector in which a promoter to control transcription of the inserted DNA has been incorporated.

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10 The term "expression vector system" as used herein refers to a recombinant DNA expression vector in combination with one or more trans-acting factors that specifically influence transcription, stability, or replication of the recombinant DNA expression vector. The trans-acting factor may be expressed from a co-transfected plasmid, virus, or other extrachromosomal element, or may be expressed from a gene integrated within the chromosome.

25

15 The term "transcription" as used herein refers to the process whereby information contained in a nucleotide sequence of DNA is transferred to a complementary RNA sequence.

30

30 The term "transfection" as used herein refers to the taking up of an expression vector by a host cell whether or not any coding sequences are in fact expressed. Numerous methods of transfection are known to the ordinarily skilled artisan, for example, calcium phosphate co-precipitation, and electroporation. Successful transfection is generally recognized when any indication of the operation of this vector occurs within the host cell.

40

40 The term "transformation" as used herein means the introduction of DNA into an organism so that the DNA is replicable, either as 45 an extrachromosomal element or by chromosomal integration. Methods of transforming bacterial and eukaryotic hosts are well known in the art, many of which methods, such as nuclear injection, protoplast fusion or by calcium treatment using calcium chloride are summarized in J. Sambrook, et al.,

MOLECULAR CLONING: A LABORATORY MANUAL, (1989).

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The term "translation" as used herein refers to the process whereby the genetic information of messenger RNA is used to specify and direct the synthesis of a polypeptide chain.

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The term "vector" as used herein refers to a nucleic acid

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- 5 compound used for the transformation of cells in gene manipulation bearing polynucleotide sequences corresponding to appropriate protein molecules which when combined with appropriate control sequences confer specific properties on the host cell to be transformed. Plasmids, viruses, and bacteriophage are suitable vectors. Artificial vectors are constructed by
- 10 cutting and joining DNA molecules from different sources using restriction enzymes and ligases. The term "vector" as used herein includes Recombinant DNA cloning vectors and Recombinant DNA expression vectors.

25

The terms "complementary" or "complementarity" as used herein refer to the capacity of purine and pyrimidine nucleotides to associate

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- 15 through hydrogen bonding to form double stranded nucleic acid molecules.

The following base pairs are related by complementarity: guanine and cytosine; adenine and thymine; and adenine and uracil. As used herein, "complementary" means that the aforementioned relationship applies to substantially all base pairs comprising two single-stranded nucleic acid

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- 20 molecules over the entire length of said molecules. "Partially complementary" refers to the aforementioned relationship in which one of two single-stranded nucleic acid molecules is shorter in length than the other such that a portion of one of the molecules remains single-stranded.

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The term "hybridization" as used herein refers to a

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- 25 process in which a strand of nucleic acid joins with a complementary strand through base pairing. The conditions employed in the hybridization of two completely or nearly completely complementary nucleic acid strands varies with the degree of complementarity of the two strands and the length of the strands. Such techniques and conditions are well known to practitioners in
- 30 this field.

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10 "Isolated amino acid sequence" refers to any amino acid sequence, however constructed or synthesized, which is locationally distinct from the naturally occurring sequence.

15 5 "Isolated DNA compound" refers to any DNA sequence, however constructed or synthesized, which is locationally distinct from its natural location in genomic DNA.

15 "Isolated nucleic acid compound" refers to any RNA or DNA sequence, however constructed or synthesized, which is locationally distinct from its natural location.

20 10 A "primer" is a nucleic acid fragment which functions as an initiating substrate for enzymatic or synthetic elongation.

25 The term "promoter" refers to a DNA sequence which directs transcription of DNA to RNA.

30 15 A "probe" as used herein is a nucleic acid compound or a fragment thereof which hybridizes with a nucleic acid compound which encodes either the entire sequence of SEQ ID NO:2 or SEQ ID NO:4, a sequence complementary to SEQ ID NO:2 or SEQ ID NO:4, or a part thereof.

35 20 The term "EST" or "expressed sequence tag" refers to a fragment or sampling of cDNA which encodes a polypeptide of unknown function.

40 25 The term "stringency" refers to a set of hybridization conditions which may be varied in order to vary the degree of nucleic acid affinity for other nucleic acid. (See the definition of "hybridization", supra.)

45 30 The term "antigenically distinct" as used herein refers to a situation in which antibodies raised against an epitope of the proteins of the present invention, or a fragment thereof, may be used to differentiate between the proteins of the present invention and other β -secretase variants. This term may also be employed in the sense that such antibodies may be used to differentiate between the human β -secretase protein and analogous proteins derived from other species.

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- 25 -

10 The term "PCR" as used herein refers to the widely-known polymerase chain reaction employing a thermally-stable polymerase. This technique, as appreciated by those skilled in the art, is employed to amplify a particular nucleic acid fragment.

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15 The term "BLAST" as used herein refers to the widely known basic local alignment search tool. This tool consists of a set of computer-based programs designed to permit examination of amino acid and nucleic acid sequence databases for similarity with an isolated sequence of interest.

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20 The term "RACE" refers to the widely known rapid amplification of complimentary ends technique, to amplify and obtain the 5' and 3' ends of isolated cDNA.

20

25 Skilled artisans will recognize that the proteins of the present invention can be synthesized by a number of different methods. All of the amino acid compounds of the invention can be made by chemical methods 15 well known in the art, including solid phase peptide synthesis, or recombinant methods. Both methods are described in U.S. Patent 4,617,149, 30 herein incorporated by reference.

25

35 The principles of solid phase chemical synthesis of polypeptides are well known in the art and may be found in general texts in the area. See, 20 e.g., H. Dugas and C. Penney, BIOORGANIC CHEMISTRY, (1981) Springer-Verlag, New York, pgs. 54-92. For examples, peptides may be synthesized by solid-phase methodology utilizing an Applied Biosystems 430A peptide synthesizer (commercially available from Applied Biosystems, Foster City 40 California) and synthesis cycles supplied by Applied Biosystems. Protected 25 amino acids, such as *t*-butoxycarbonyl-protected amino acids, and other reagents are commercially available from many chemical supply houses.

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45 Sequential *t*-butoxycarbonyl chemistry using double couple protocols are applied to the starting *p*-methyl benzhydryl amine resins for the production of C-terminal carboxamides. For the production of C-terminal 50 acids, the corresponding pyridine-2-aldoxime methiodide resin is used.

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Asparagine, glutamine, and arginine are coupled using preformed hydroxy benzotriazole esters. The following side chain protection may be used:

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Arg, Tosyl
Asp, cyclohexyl

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Glu, cyclohexyl
Ser, Benzyl

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Thr, Benzyl
Tyr, 4-bromo carbobenzoxy

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- Removal of the *t*-butoxycarbonyl moiety (deprotection) may be accomplished with trifluoroacetic acid (TFA) in methylene chloride. Following completion of the synthesis the peptides may be deprotected and cleaved from the resin with anhydrous hydrogen fluoride containing 10% meta-cresol. Cleavage of the side chain protecting group(s) and of the peptide from the resin is carried out at zero degrees centigrade or below, preferably 15 20°C for thirty minutes followed by thirty minutes at 0°C.

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After removal of the hydrogen fluoride, the peptide/resin is washed with ether, and the peptide extracted with glacial acetic acid and then lyophilized. Purification is accomplished by size-exclusion chromatography on a Sephadex G-10 (Pharmacia) column in 10% acetic acid.

35

- The proteins of the present invention may also be produced by recombinant methods. Recombinant methods are preferred if a high yield is desired. A general method for the construction of any desired DNA sequence is provided in J. Brown, et al., Methods in Enzymology, 68:109 (1979). See also, J. Sambrook, et al., supra.

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- 25 The basic steps in the recombinant production of desired proteins are:

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- 30 a) construction of a synthetic or semi-synthetic DNA encoding the protein of interest;

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b) integrating said DNA into an expression vector in a manner suitable for the expression of the protein of interest, either alone or as a fusion protein;

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c) transforming an appropriate eukaryotic or prokaryotic host cell with said expression vector;

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d) culturing said transformed or transfected host cell in a manner to express the protein of interest; and

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e) recovering and purifying the recombinantly produced protein of interest.

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In general, prokaryotes are used for cloning of DNA sequences in constructing the vectors of this invention. Prokaryotes may also be employed in the production of the protein of interest. For example, the Escherichia coli K12 strain 294 (ATCC No. 31446) is particularly useful for the prokaryotic expression of foreign proteins. Other strains of E. coli which may be used (and their relevant genotypes) include the following.

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Strain	Genotype
DH5a	F ⁻ (λ80dlacZDM15), D(lacZYA-argF)U169 supE44, l ⁻ , hsdR17(rK ⁻ , mK ⁺), recA1, endA1, gyrA96, thi-1, relA1
HB101	supE44, hsdS20(rB ⁻ mB ⁻), recA13, ara-14, proA2 lacY1, galK2, rpsL20, xyl-5, mtl-1, mcrB, mrr

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JM109

recA1, e14⁻(mcrA), supE44, endA1,
hsdR17(r_K⁻, m_K⁺), gyrA96, relA1, thi-1, (lac-
proAB), F'[traD36, proAB+ lacI^q, lacZ?M15]

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RR1

supE44, hsdS20(r_B⁻ m_B⁺), ara-14 proA₂,
lacY1, galK2, rpsL20, xyl-5, mtl-5

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c1776

F⁻, ton, A53, dapD8, minA1, supE42
(glnV42), D(gal-uvrB)40, minB2, rfb-2,
gyrA25, thyA142, oms-2, metC65, oms-1,
D(bioH-asd)29, cycB2, cycA1, hsdR2, l-

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294

endA, thi, hsr, hsm_k⁺ (U.S. Patent
4,366,246)

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LE392

F⁻, hsdR514 (r^rm^m), supE44, supF58, lacY1,
or Dlac(l-Y)6, galK2, glaT22, metB1, trpR55,
l-

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These strains are all commercially available from suppliers such
as: Bethesda Research Laboratories, Gaithersburg, Maryland 20877 and
Stratagene Cloning Systems, La Jolla, California 92037; or are readily

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- available to the public from sources such as the American Type Culture
Collection, 12301 Parklawn Drive, Rockville, Maryland, 10852-1776. Except
where otherwise noted, these bacterial strains can be used interchangeably.
The genotypes listed are illustrative of many of the desired characteristics for
choosing a bacterial host and are not meant to limit the invention in any way.
- 10 The genotype designations are in accordance with standard nomenclature.
See, for example, J. Sambrook, et al., supra.

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In addition to the strains of E. coli discussed supra, bacilli such as Bacillus subtilis, other enterobacteriaceae such as Salmonella typhimurium or Serratia marcescens, and various Pseudomonas species may be used. In addition to these gram-negative bacteria, other bacteria, especially Streptomyces, spp., may be employed in the prokaryotic cloning and expression of the proteins of this invention.

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Promoters suitable for use with prokaryotic hosts include the b-lactamase [vector pGX2907 (ATCC 39344) contains the replicon and b-lactamase gene] and lactose promoter systems [Chang et al., Nature (London), 275:615 (1978); and Goeddel et al., Nature (London), 281:544 (1979)], alkaline phosphatase, the tryptophan (trp) promoter system [vector PATH1 (ATCC 37695) is designed to facilitate expression of an open reading frame as a trpE fusion protein under control of the trp promoter] and hybrid promoters such as the tac promoter (isolatable from plasmid pDR540 ATCC-37282). However, other functional bacterial promoters, whose nucleotide sequences are generally known, enable one of skill in the art to ligate them to DNA encoding the proteins of the instant invention using linkers or adapters to supply any required restriction sites. Promoters for use in bacterial systems also will contain a Shine-Dalgarno sequence operably linked to the DNA encoding the desired polypeptides. These examples are illustrative rather than limiting.

The proteins of this invention may be synthesized either by direct expression or as a fusion protein comprising the protein of interest as a translational fusion with another protein or peptide which may be removable by enzymatic or chemical cleavage. It is often observed in the production of certain peptides in recombinant systems that expression as a fusion protein prolongs the lifespan, increases the yield of the desired peptide, or provides a convenient means of purifying the protein of interest. A variety of peptidases (e.g. trypsin) which cleave a polypeptide at specific sites or digest the peptides from the amino or carboxy termini (e.g. diaminopeptidase) of the peptide

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chain are known. Furthermore, particular chemicals (e.g. cyanogen bromide) will cleave a polypeptide chain at specific sites. The skilled artisan will appreciate the modifications necessary to the amino acid sequence (and synthetic or semi-synthetic coding sequence if recombinant means are employed) to incorporate site-specific internal cleavage sites. See e.g., P. Carter, "Site Specific Proteolysis of Fusion Proteins", Chapter 13 in PROTEIN PURIFICATION: FROM MOLECULAR MECHANISMS TO LARGE SCALE PROCESSES, American Chemical Society, Washington, DC (1990).

20

In addition to cloning and expressing the genes of interest in the prokaryotic systems discussed above, the proteins of the present invention may also be produced in eukaryotic systems. The present invention is not limited to use in a particular eukaryotic host cell. A variety of eukaryotic host cells are available from depositories such as the American Type Culture Collection (ATCC) and are suitable for use with the vectors of the present invention. The choice of a particular host cell depends to some extent on the particular expression vector used to drive expression of the amyloid precursor protein protease-encoding nucleic acids of the present invention. Exemplary host cells suitable for use in the present invention are listed in Table I. These exemplary host cells are merely illustrative of the many eukaryotic cells available for use with the present invention and are not meant in any way to limit the scope of the present invention.

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Table I

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Host Cell	Origin	Source
HepG-2	Human Liver Hepatoblastoma	ATCC HB 8065
CV-1	African Green Monkey Kidney	ATCC CCI. 70
LLC-MK ₂	Rhesus Monkey Kidney	ATCC CCL 7
3T3	Mouse Embryo Fibroblasts	ATCC CCL 92
CHO-K1	Chinese Hamster Ovary	ATCC CCL 61
HeLa	Human Cervix Epitheloid	ATCC CCL 2

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	RPMI8226	Human Myeloma	ATCC CCL 155
	H4IIEC3	Rat Hepatoma	ATCC CCL 1600
10	C127I	Mouse Fibroblast	ATCC CCL 1616
	293	Human Embryonal Kidney	ATCC CRL 1573
	Sf9	Fall armyworm ovary <u>Spodoptera frugiperda</u>	ATCC CRL-1711
15	HS-Sultan	Human Plasma Cell Plasmacytoma	ATCC CCL 1484
	BHK-21	Baby Hamster Kidney	ATCC CCL 10

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A preferred cell line employed in the expression of the protein of the present invention is the widely available 293 cell line. As noted, this cell line was constructed from human embryonal kidney tissue and is available from American Type Culture Collection under the accession number ATCC CCL 1573.

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A wide variety of vectors, some of which are discussed below, exists for the transformation of mammalian host cells, but the specific vectors described herein are merely illustrative and are in no way intended to limit the scope of the present invention.

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Some illustrative vectors include the pSV2-type vectors which comprise segments of the simian virus 40 (SV40) genome that constitute a defined eukaryotic transcription unit-promoter, intervening sequence, and polyadenylation site. In the absence of the SV40 T antigen, the plasmid pSV2-type vectors transform mammalian and other eukaryotic host cells by integrating into the host cell chromosomal DNA. A large number of plasmid pSV2-type vectors have been constructed, such as plasmid pSV2-gpt, pSV2-neo, pSV2-dhfr, pSV2-hyg, and pSV2-b-globin, in which the SV40 promoter drives transcription of an inserted gene. These vectors are suitable for use with the coding sequences of the present invention and are widely available

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from sources such as the ATCC or the Northern Regional Research Laboratory (NRRL), 1815 N. University Street, Peoria, Illinois, 61604.

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The plasmid pSV2-dhfr (ATCC 37146) comprises a murine dihydrofolate reductase (dhfr) gene under the control of the SV40 early promoter. Under the appropriate conditions, the dhfr gene is known to be amplified, or copied, in the host chromosome. This amplification can result in the amplification of closely-associated DNA sequences and can, therefore, be used to increase production of a protein of interest. See, e.g., J. Schimke, Cell, 35:705-713 (1984).

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10 Plasmids constructed for expression of the proteins of the present invention in mammalian and other eukaryotic host cells can utilize a wide variety of promoters. The present invention is in no way limited to the use of the particular promoters exemplified herein. Promoters such as the SV40 late promoter, promoters from eukaryotic genes, such as, for example, 25 the estrogen-inducible chicken ovalbumin gene, the interferon genes, the gluco-corticoid-inducible tyrosine aminotransferase gene, and the thymidine kinase gene, and the major early and late adenovirus genes can be readily isolated and modified to express the genes of the present invention. 30 Eukaryotic promoters can also be used in tandem to drive expression of a coding sequence of this invention. Furthermore, a large number of retroviruses are known that infect a wide range of eukaryotic host cells. The long terminal repeats in the retroviral DNA frequently encode functional 35 promoters and, therefore, may be used to drive expression of the nucleic acids of the present invention.

25 Plasmid pRSVcat (ATCC 37152) comprises portions of a long terminal repeat of the Rous Sarcoma virus, a virus known to infect chickens and other host cells. This long terminal repeat contains a promoter which is 40 suitable for use in the vectors of this invention. H. Gorman, et al., Proceedings of the National Academy of Sciences (USA), 79:6777 (1982). The 45 30 plasmid pMSVi (NRRL B-15929) comprises the long terminal repeats of the

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- 33 -

Murine Sarcoma virus, a virus known to infect mouse and other host cells.

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The mouse metallothionein promoter has also been well characterized for use in eukaryotic host cells and is suitable for use in the expression of the nucleic acids of the present invention. The mouse metallothionein promoter is

15

5 present in the plasmid pdBPV-MMneo (ATCC 37224) which can serve as the starting material of other plasmids of the present invention.

20

Another usefull expression vector system employs one of a series of vectors containing the BK enhancer, an enhancer derived from the BK virus, a human papovavirus. The most preferred such vector systems are

25

10 those which employ not only the BK enhancer but also the adenovirus-2-early region 1A (E1A) gene product. The E1A gene product (actually, the E1A gene produces two products, which are collectively referred to herein as "the E1A gene product") is an immediate-early gene product of adenovirus, a large DNA virus.

30

15 An additional useful eukaryotic expression vector is the phd series of vectors which comprise a BK enhancer in tandem with the adenovirus late promoter to drive expression of useful products in eukaryotic host cells. The construction and method of using the phd plasmid, as well as related plasmids, are described in U.S. Patents 5,242,688, issued September

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20 7, 1993, and 4,992,373, issued February 12, 1991, all of which are herein incorporated by reference. Escherichia coli K12 GM48 cells harboring the plasmid phd are available as part of the permanent stock collection of the Northern Regional Research Laboratory under accession number NRRL B-18525. The plasmid may be isolated from this culture using standard

40

25 techniques.

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The plasmid phd contains a unique BclI site which may be utilized for the insertion of the gene encoding the protein of interest. The skilled artisan understands that linkers or adapters may be employed in cloning the gene of interest into this BclI site. The phd series of plasmids

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30 functions most efficiently when introduced into a host cell which produces the

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E1A gene product, cell lines such as AV12-664, 293 cells, and others, described supra.

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Transformation of the mammalian cells can be performed by any of the known processes including, but not limited to, the protoplast fusion method, the calcium phosphate co-precipitation method, electroporation and the like. See, e.g., J. Sambrook, et al., supra, at 3:16.30-3:16.66.

15

Other routes of production are well known to skilled artisans. In addition to the plasmid discussed above, it is well known in the art that some viruses are also appropriate vectors. For example, the adenovirus, the adenovirus-associated virus, the vaccinia virus, the herpes virus, the baculovirus, and the rous sarcoma virus are useful. Such a method is described in U.S. Patent 4,775,624, herein incorporated by reference. Several alternate methods of expression are described in J. Sambrook, et al., supra, at 16.3-17.44.

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In addition to prokaryotes and mammalian host cells, eukaryotic microbes such as yeast cultures may also be used. The imperfect fungus Saccharomyces cerevisiae, or common baker's yeast, is the most commonly used eukaryotic microorganism, although a number of other strains are commonly available. For expression in Saccharomyces sp., the plasmid YRp7 (ATCC-40053), for example, is commonly used. See, e.g., L. Stinchcomb, et al., Nature (London), 282:39 (1979); J. Kingsman et al., Gene, 7:141 (1979); S. Tschemper et al., Gene, 10:157 (1980). This plasmid already contains the trp gene which provides a selectable marker for a mutant strain of yeast lacking the ability to grow in tryptophan.

25

Suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase [found on plasmid pAP12BD (ATCC 53231) and described in U.S. Patent No. 4,935,350, issued June 19, 1990, herein incorporated by reference] or other glycolytic enzymes such as enolase [found on plasmid pAC1 (ATCC 39532)], glyceraldehyde-3-phosphate dehydrogenase [derived from plasmid pHcGAPC1 (ATCC 57090, 57091)], hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-

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phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase,
triosephosphate isomerase, phosphoglucose isomerase, and glucokinase, as
well as the alcohol dehydrogenase and pyruvate decarboxylase genes of
Zymomonas mobilis (United States Patent No. 5,000,000 issued March 19,

5 1991, herein incorporated by reference).

15

Other yeast promoters, which are inducible promoters, having
the additional advantage of their transcription being controllable by varying
growth conditions, are the promoter regions for alcohol dehydrogenase 2,
isocytchrome C, acid phosphatase, degradative enzymes associated with
20 nitrogen metabolism, metallothionein [contained on plasmid vector
pCL28XholLHPV (ATCC 39475) and described in United States Patent No.
4,840,896, herein incorporated by reference], glyceraldehyde 3-phosphate
25 dehydrogenase, and enzymes responsible for maltose and galactose [e.g.
GAL1 found on plasmid pRY121 (ATCC 37658)] utilization. Suitable vectors
15 and promoters for use in yeast expression are further described in R.
Hitzeman *et al.*, European Patent Publication No. 73,657A. Yeast enhancers
30 such as the UAS Gal from Saccharomyces cerevisiae (found in conjunction
with the CYC1 promoter on plasmid YEpsec-h11beta ATCC 67024), also are
advantageously used with yeast promoters.

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20 Practitioners of this invention realize that, in addition to the
above-mentioned expression systems, cloned cDNA may also be employed in
the production of transgenic animals in which a test mammal, usually a
40 mouse, in which expression or overexpression of the proteins of the present
invention can be assessed. The nucleic acids of the present invention may
25 also be employed in the construction of "knockout" animals in which the
expression of the native cognate of the gene is suppressed.

45

Skilled artisans will recognize that the protease of the present
invention, as well as the nucleic acid compounds encoding said protease, can
be isolated and purified from cultured host cells transiently expressing β -
50 secretase activity. The following examples further illustrate such isolation

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- 36 -

and purification processes, however, these examples are not in any way to be interpreted as limiting the scope of the present invention.

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Isolation and Purification of β -secretase

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Example 1

293 Cell Source

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293 Cells were obtained as by-products from 25- to 30-day fermentations at Lilly Technology Center. (Eli Lilly and Co., Indianapolis, IN.)

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Example 2

β -Secretase Activity Assay

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The enzymatic activity of beta-secretase was determined by an ELISA assay, modified in form over an assay appearing in application No.

- 15 PCT/US96/09985, the entire content of which is herein incorporated by reference. Using MBP-APPc125sw as the substrate, the activity was determined by measuring the MBP-APPc26sw cleavage product with a polyclonal antibody, 192sw, highly specific to the product. MBP-APPc125sw is a fusion substrate in which maltose binding protein is fused to the 125-residue C-terminal portion of the swedish amyloid precursor protein. For the enzymatic activity analysis, one picounit (pU) is defined as the amount of the enzyme that catalyzes the conversion of MBP-APP125sw to one picomole of MBP-APPc26sw per ml in 2-hr under the optimized reaction conditions of the Elisa assay (see Table II, infra). To calculate the enzyme specific activity, the protein concentration was first determined using the well known Bio-Rad microassay method. (Rio-Rad Laboratories, Hercules, CA, 94547)

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Example 3
β-Secretase Purification

15 5 The purification of beta-secretase was carried out by a protocol
modified over the purification methods appearing in application No.
PCT/US96/09985, the entire content of which is herein incorporated by
reference. The enzyme purification protocol was undertaken at 4 C. β-
Secretase activity and protein recovery data are provided in Table III, infra.

20 10 **Step 1:**
25 Membrane Extract: About 400-g of 293 cells were resuspended in 2,000-ml
of 20 mM HEPES (Sigma Chemical Co., St Louis, MO), pH 7.5, 2 mM EDTA
(Sigma Chemical Co., St Louis, MO) and 0.25% sucrose (Buffer 1A). The cell
30 15 suspension was homogenized in an 1000-ml aliquot and the cells were broken
with an Brinkmann Homogenizer (POLYTRON, Switzerland) according to
the following conditions: at setting 4 for 2- and 1-min; and at setting 5 for 1-
35 20 and 0.5-min (with 3-min cooling time after each homogenization). The broken
cell suspension was centrifuged at 1,000xg for 20-min; the resulting
supernatant (post-nuclear supernatant; PNS1) was saved. The pellet was
resuspended in 1,200-ml of Buffer 1A, homogenized, broken and centrifuged
as described above; the supernatant (PNS2) was saved and the pellet was
discarded. PNS1 and PNS2 were combined (2,700-ml) and centrifuged at
40 40 45,000xg for 1-hr; the resulting pellet (P2; containing membranes) was saved
and the supernatant was discarded. This pellet was resuspended in 3,200-ml
45 45 of 20 mM MES (Sigma Chemical Co., St Louis, MO), pH 6.0, 2 mM EDTA,
0.5% Triton X-100, 150 mM NaCl, 0.2 mM AEBSF, 5 mg/ml leupeptin, 2
mg/ml E64 and 1 mg/ml pepstatin A (Buffer 1B); all four protease inhibitors
were from Calbiochem; San Diego, CA). The suspension was stirred
50 50 continuously for 1-hr for extraction of beta-secretase and centrifuged at

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16,000xg for 1-hr; the pellet was discarded. The resulting supernatant (3,120-ml) was adjusted to pH 7.5 with 1 M Tris base and filtered through 0.45-mm Zapcap-S (Schleicher & Schuell; Keene, NH); the filtrate was the P2 membrane extract (P2ME, 3,170-ml).

15

A second P2ME was prepared similarly from another 400g of 293 cells. The combined beta-secretase activity and protein data for the P2ME fractions are shown in Table III. However, beta-secretase activity from each P2ME was purified separately in the next step.

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Step 2:

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Wheat Germ Agglutinin (WGA) Agarose Eluate: The first P2ME was loaded to a WGA-Agarose column (Vector Lab.; Burlingame, CA) (1000-ml), pre-equilibrated with 1500-ml of 20 mM Tris, pH 7.5, 2 mM EDTA, 0.5%

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15 Triton X-100 and 150 mM NaCl (Buffer 2A). The WGA column, which binds to N-acetyl-D-glucosamine glycopeptides, was washed with 1000-ml of Buffer 2A and bound proteins were eluted with a linear gradient of 0-10% chitin hydrolysate (Vector Lab.) in a total volume of 900-ml constructed from Buffer 2A and Buffer 2B (20 mM Tris, pH 7.5, 2 mM EDTA, 0.5% Triton X-100 and 20 10% chitin hydrolysate). The fractions containing higher specific activities of beta-secretase were pooled as the WGA-eluate (180-ml).

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40 The WGA-Agarose column was regenerated and equilibrated. The second WGA-eluate (170-ml) was obtained similarly from the second P2ME. The two 25 WGA-eluates were combined.(see Table III). In addition, the two WGA-Agarose washings were combined.(see Table III). The WGA-eluate and the 45 WGA-wash were purified together in the next step.

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Step 3:

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HiTrap Q (HiQ) Eluate: The WGA-eluate and the WGA-wash were diluted 6x and 4x, respectively, with 20 mM Tris, pH 8.0, 2 mM EDTA and 0.2%

15 5 Triton X-100 (Buffer 3A) to reduce Triton X-100 and NaCl concentrations.

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Both diluted enzyme preparations were loaded consecutively to four connected, fast flow anion exchanger HiTrap Q columns (4x5-ml; Amersham Pharmacia Biotech, Piscataway, NJ), pre-equilibrated with 100-ml of Buffer 3A, and the column was washed with 200-ml of Buffer 3A. Bound proteins 20 10 were eluted first with a linear gradient of 0-500 mM NaCl in buffer 3A in a total volume of 420-ml and then eluted with 100-ml of Buffer 3B (Buffer 3A plus 500 mM NaCl). The fractions containing higher specific activities were 25 25 pooled as the HiQ-eluate.(Table III) The HiQ-eluate was used directly in the next step.

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Step 4:

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Hydroxylapatite (HA) Wash: The HiQ-eluate was loaded to a Hydroxylapatite column (10-ml; Bio-Rad, Hercules, CA), pre-equilibrated with 100-ml of Buffer 4A (same as Buffer 3A), the column flow-through was 35 20 collected. HA separation of proteins is based on charge absorption and desorption. The column was washed with 50-ml of Buffer 4A, and the bound proteins were eluted from the column with a linear gradient of 0-500 mM potassium phosphate in Buffer 4A in a total volume of 100-ml. Among the 40 40 three fractions (the flow-through, the wash, and the eluate), the HA-wash 25 25 (50-ml) showed the highest total , and specific activity of beta-secretase (Table III) and, thus, was used in the next step.

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Step 5:

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Mono Q Eluate. The HA-wash was de-salted to about 15 mM NaCl with 30 Buffer 5A (same as Buffer 4A) using Centriprep 50 (Millipore, Bedford, MA).

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The de-salted HA-wash was loaded to a high resolving strong anion exchanger Mono Q column (1-ml; Amersham Pharmacia Biotech), pre-equilibrated with 30-ml of Buffer 5A. The column was washed with 30-ml of buffer 5A, and bound proteins were eluted first with a linear gradient of 0-500 mM in Buffer 5A in a total volume of 20-ml and then eluted with 10-ml of Buffer 5B (Buffer 5A plus 500 mM NaCl). Two activity peaks were observed and the active fractions from each activity peak were pooled.(Table III) The two Mono Q-eluates (2-ml & 4-ml)were purified separately in the next step.

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10 Step 6:

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Superdex (S) 200 Eluate. Mono Q-eluate 1 was loaded to a high resolution gel-filtration Superdex 200 column (300-ml; Amersham Pharmacia Biotech), pre-equilibrated with 900-ml of 20 mM Tris, pH 8.0, 2 mM EDTA, 0.2% Triton X-100, 1 mM MgCl₂, 1 mM CaCl₂ and 150 mM NaCl (Buffer 6). The proteins were eluted with 300-ml of Buffer 6. Two activity peaks were observed and the active fractions from both peaks were pooled together (S-200-eluate 1, 19.2-ml)(Table III) and used in the next step. Mono Q-eluate 2 was similarly purified by the same Superdex 200 column; three activity peaks were observed. The two Superdex 200-eluates that showed the higher specific activities (S-200 eluates 2a & 2b; Table III) were used separately in the next step.

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Step 7:

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DEAE Eluate. S-200-eluates 1 and 2a were de-salted with a Sepharose G-25 column (100-ml; Amersham Pharmacia Biotech) and S-200-eluate 2b was diluted 6x with Buffer 7A (same as 5A) to 25 mM NaCl.. To the resulting S-200-eluates; 200-, 200- and 100 µl of DEAE-Sepharose was added, respectively. For effective binding of the activity to the resin, the three samples were agitated continuously overnight. The samples were centrifuged at 10,000xg for 10-min to collect DEAE-Sepharose beads. The bound proteins

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were eluted from DEAE-Sephadose beads of the three samples with, respectively, 2x200-, 2x400- and 2x100 µl of Buffer 7B (Buffer 7A plus 1 M NaCl). The three DEAE-eluates (400-, 800-, and 200 µl; Table III) were treated separately in the next step.

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Step 8:

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De-Glycosylation. To each of the three DEAE-eluates, beta-mercaptoethanol (reducing agent) was added to a final concentration of 3 mM. PNGase F (100 mU/40-ml from Glyko, Novato, CA); an N-linked de-glycosylation enzyme, was added as three aliquots to each sample to a final ratio of about 1:4 (V/V). After each PNGase addition, the samples were placed in a 37 °C incubator for one day. After a total incubation time of three days, beta-secretase activity was stable in two samples and there was a slight (about 20%) activity loss in the other sample (Table III). The three samples (De-Gly) were purified separately in the next and last step.

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Step 9:

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Mini Q Eluate. Each of the three De-Gly samples was de-salted with a Sephadex PD-10 column (Amersham Pharmacia Biotech). Desalting De-Gly sample 1 was loaded to a Mini Q PE column (0.8-ml from Amersham Pharmacia Biotech), a high resolving anion exchanger, pre-equilibrated with Buffer 9 A (same as Buffer 7A). The bound proteins were washed and eluted with a step-wise NaCl gradient in Buffer 7A in a total volume of 35.6-ml as shown below: 7.6-ml at 0 mM NaCl, 16-ml from 0 to 250 mM, 8-ml from 250 to 500 mM and 4-ml at 500 mM. Two activity peaks were observed. Desalting De-Gly 2a were purified in a similar way; two activity peaks were also observed. Desalting De-Gly 2b sample was purified with a Mini Q PC column (0.24-ml from Amersham Pharmacia Biotech) using a step-wise NaCl gradient in Buffer 7A in a total volume of 13.2-ml (4.8-ml at 0 mM NaCl, 4.8-ml from 0 to 250 mM, 2.4-ml from 250 to 500 mM and 1.2-ml at 500 mM).

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Only one major activity peak was observed. The resulting beta-secretase activity and protein data are shown in Table III.

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Beta-secretase activity was purified up to 3,000-fold to apparent homogeneity by the 9-step procedure. Note, however, that the actual activity enrichment was likely much greater excluding Triton X-100 interference to the low level protein determination in Step 9 above.

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Table II
Optimized Assay for β -Secretase Activity

	Assay Parameter	Optimized Activity Conditions
15	Enzyme*	0.015-0.095 pU for Linear Response (With 0.02 to 0.06 % Triton X-100)
30	Substrate	~60 nM for Maximal Activity (With ~20 mM Guanidine HCl)
20	pH	5.25 to 5.75 for Maximal Activity
35	Reaction Time	\geq 4 hours for Linear Response
40	Kinetic Constants	
	K_m	300 nM
	V_{max}	2 nmol/hr/mg protein

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*Using 0.313- μ l of Mini Q-Eluate 2a .

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Note: The enzymatic reaction was carried out at room temperature.
The purified enzyme was stable at 4 or -20 C for at least two weeks.

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Table III

	Fraction (step)	Total Activity (pU)	Total Protein (mg)	Sp. Act. (pU/mg)	Recovery (%)
10					
15	P2ME (1)	35,038	23,245	1,507	100
20	WGA-Wash (2)	2,160	206	10.49	6
	WGA-E* (2)	8,330	652	12.78	24
25	HiQ-E* (3)	5,998	259	23.16	17
	HA-Wash (4)	2,550	20.4	125.0	7.3
30	Mono Q-E*1 (5)	1,248	3.99	312.7	3.6
	Mono Q-E*2 (5)	2,240	6.43	348.4	6.4
35	S-200-E*1 (6)	199.5	0.90	221.7	0.6
	S-200-E*2b (6)	386.5	1.54	251.0	1.1
	S-200-E*2c (6)	60.0	0.16	375.0	0.2
40	DEAE-E*1 (7)	239.3	0.406	574.5	0.7
	DEAE-E*2 (7)	771.8	0.642	1202	2.2
	DEAE-E*3 (7)	8.35	0.048	174.0	—
45	De-Gly*1 (8)	222.5	0.397	560.5	0.6
	De-Gly*2 (8)	534.3	0.634	842.7	1.5
	De-Gly*3 (8)	11.33	0.046	246.2	—
50	Mini Q-E*1a (9)	121.8	0.049	2485	0.3
	Mini Q-E*1b (9)	76.8	0.045	1706	0.2
	Mini Q-E*2a (9)	247.0**	0.087	2839	0.7
	Mini Q-E*2b (9)	369.8**	0.121	3056	1.1
	Mini Q-E*3 (9)	2.95	0.009	327.8	—

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*E = Eluate; FT = Flow-Through; De-Gly = De-Glycosylated

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** Mini Q-E 1a and Mini Q-E 1b each contained two activity peaks.

5 Mini Q-Eluate 2a represents the first peak from fraction Q-E 1a combined with the first peak from fraction

15 Q-E 1b.

Mini Q-Eluate 2b represents the second peak from fraction Q-E 1a combined with the second peak from fraction Q-E 1b.

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Skilled artisans will recognize that some alterations of SEQ ID

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NO:2 or SEQ ID NO:4 will fail to change the function of the amino acid compound. For instance, some hydrophobic amino acids may be exchanged for other hydrophobic amino acids. Those altered amino acid compounds

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15 which confer substantially the same function in substantially the same manner as the exemplified amino acid compounds are also encompassed within the present invention. Typical such conservative substitutions attempt to preserve the: (a) secondary or tertiary structure of the polypeptide backbone; (b) the charge or hydrophobicity of the residue; or (c) the bulk of 20 the side chain. Some examples of such conservative substitutions of amino acids, resulting in the production of proteins which are functional equivalents 30 of the protein of SEQ ID NO:2 or SEQ ID NO:4 are shown in Table II, infra.

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Table IV

		Original Residue	Exemplary Substitutions
10		Ala	Ser, Gly
		Arg	Lys
15	5	Asn	Gln, His
		Asp	Glu
		Cys	Ser
		Gln	Asn
20		Glu	Asp
	10	Gly	Pro, Ala
		His	Asn, Gln
25		Ile	Leu, Val
		Leu	Ile, Val
		Lys	Arg, Gln, Glu
30	15	Met	Leu, Ile
		Phe	Met, Leu, Tyr
		Ser	Thr
		Thr	Ser
35		Trp	Tyr
	20	Tyr	Trp, Phe
		Val	<u>Ile, Leu</u>

40

These substitutions may be introduced into the protein in a variety of ways, such as during the chemical synthesis or by chemical modification of an amino acid side chain after the protein has been prepared.

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Alterations of the protein having a sequence which corresponds to the sequence of SEQ ID NO:2 or SEQ ID NO:4 may also be induced by alterations of the nucleic acid compounds which encodes these proteins.

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These mutations of the nucleic acid compound may be generated by either

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random mutagenesis techniques, such as those techniques employing chemical mutagens, or by site-specific mutagenesis employing oligonucleotides. In addition, allelic variants of the gene encoding the protein of the present invention may also be purified by the processes of the present invention. Those nucleic acid compounds which confer substantially the same function in substantially the same manner as the exemplified nucleic acid compounds are also encompassed within the present invention.

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Other embodiments of the present invention include nucleic acid compounds which comprise isolated nucleic acid sequences which encode SEQ ID NO:2 or SEQ ID NO:4. As skilled artisans will recognize, the amino acid compounds of the invention can be encoded by a multitude of different nucleic acid sequences because most of the amino acids are encoded by more than one nucleic acid triplet due to the degeneracy of the amino acid code. Because these alternative nucleic acid sequences would encode the same amino acid sequences, the present invention further comprises these alternate nucleic acid sequences.

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The full length nucleic acid clones which encode the amino acid sequences given by SEQ ID NO:2 and SEQ ID NO:4, where determined using standard methods, essentially as follows. Fractions of purified beta-secretase, as isolated by the methods described in Examples 1 through 3 above, were applied to an SDS-polyacrylamide gel. Following electrophoresis, the proteins were transferred electrophoretically to a polyvinylidene difluoride (PVDF) membrane and stained with coomassie blue. The stained protein bands were then excised from the membrane and placed in an automatic protein sequencer where the amino acid sequence of the protein was determined using widely known automated Edman chemistry. N-terminal fragments of the determined protein sequence, of approximately 17-20 amino acids, were then searched against protein sequence databases using commercially available BLAST methodology. A BLAST analysis of the proprietary INCYTE database (INCYTE Pharmaceuticals, Palo Alto, CA,

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94304) revealed a series of ESTs showing homology to the determined experimental sequence. The ESTs were subsequently assembled into a contiguous cDNA sequence.

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The transcript of the assembled ESTs, however, did not contain a starting methionine. In order to elongate the 5' end of the experimental sequence 5' RACE (rapid amplification of complimentary ends) was performed. [see generally: RACE, as described in M.A. Fohrman, PCR Protocols: A Guide to Methods and Applications, McInnis et al., Eds., Academic Press, Inc, San Diego, CA, pp. 28-29 (1990); see also U.S. Patent No. 5,470,722; and also see Ausubel et al, Current Protocols in Molecular Biology, Ch. 15, Eds.. Wiley and Sons, N.Y. (1989-1990)] After designing suitable primers based on the information contained in the EST contiguous cDNA sequence, RACE-ready cDNA (CLONTECH Laboratories, Palo Alto, CA, 94303) was used as a template to elongate and amplify the 5' end until a starting methionine was detected. PCR was then employed to generate the full length cDNA clone. *E. coli* were subsequently transformed with the full length cDNAs comprising SEQ ID NO:1 and SEQ ID NO:3 in order to generate sufficient copies of the nucleic acids for sequence determination.

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The gene encoding the amyloid precursor protein protease of the present invention may also be produced using synthetic methodology, which synthesis is well known in the art. See, e.g., E.L. Brown, R. Belagaje, M.J. Ryan, and H.G. Khorana, Methods in Enzymology, 68:109-151 (1979). Additionally, the nucleic acid sequences corresponding to the gene encoding the amyloid precursor protein protease of the present invention, can also be generated using conventional DNA synthesizing apparatuses such as the Applied Biosystems Model 380A or 380B DNA synthesizers. (commercially available from Applied Biosystems, Inc., 850 Lincoln Center Drive, Foster City, CA 94404) These synthesizers employ phosphoramidite chemistry. In the alternative, the more traditional phosphotriester chemistry may be

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employed to synthesize the nucleic acids of this invention. See, e.g., M.J. Gait, ed., OLIGONUCLEOTIDE SYNTHESIS, A PRACTICAL APPROACH, (1984).

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The synthetic amyloid precursor protein protease gene may be designed to possess restriction endonuclease cleavage sites at either end of the transcript to facilitate isolation from and integration into expression and amplification plasmids. The restriction sites are chosen so as to properly orient the coding sequence of the target enzyme with control sequences to achieve proper in-frame reading and expression of the amyloid precursor protein protease molecule. A variety of other such cleavage sites may be incorporated depending on the particular plasmid constructs employed and may be generated by techniques well known in the art.

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In an alternative methodology, the desired DNA sequences can be generated using the polymerase chain reaction as described in U.S. Patent No. 4,889,818, which is herein incorporated by reference.

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In addition to the deoxyribonucleic acid compounds described supra, the present invention also encompasses ribonucleic acid compounds which have a sequence which encodes SEQ ID NO:2 or SEQ ID NO:4. Particularly, the present invention provides the RNA sequence represented by

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GCUGUCAGC CGCCUCACAG GAAGAUGCUG CGUCCCCGGG GCAGCCCUGG 50

CAUGGGUGUG CAUGUGGGUG CAGCCCCUGGG AGCACUGUGG UUCUGCCUCA 100

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CAGGAGCCCU GGAGGUCCAG GUCCUGAAG ACCCAGUGGU GGCACUGGGUG 150

GGCACCGAUG CCACCCUGUG CUGCUCCUUC UCCCCUGAGC CUGGCUUCAG 200

45

CCUGGCCACAG CUCAACCUCA UCUGGCAGCU GACAGAUACC AACACGUGG 250

30

UGCACAGCUU UGCUGAGGGC CAGGACCAGG GCAGCGCCUA UGCCAACCGC 300

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ACGGCCCCU UCCCGGACCU GCUGGCCACAG GCCAACGCAU CCCUGAGGCCU 350

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10 GCAGGCGGUG CGUGUUGGGGG ACCAGGGCAG CUUCACCUGC UUCGGAGCA 400
 10 UCCGGGAUUU CGGCACCGCU GCGGUAGCC UGCAGGUGGC CGCUCCUAC 450
 5 UCGAAGCCC A CAUGACCCU GGAGCCAAAC AAGGACCUUGC GGCCAGGGG 500
 15 CACGGUGACC AUCACGUGCU CCAGCUACCA OGGCUACCCU GAGGCUGAGG 550
 10 UGUUUCUGGCA GGAUUGGCAG GGUGUUCCCC UGACUGGCAA CGUGACCAAG 600
 20 UCCGAGAUGG CCAACGAGCA GGGCUUGUUU GAUGUGCACA GCAUCCUGCG 650
 15 GGUGGUUGUG GGUGCAAUG GCACCUACAG CUGCCUGGU CGCAACCCCC 700
 25 UGCUGGAGCA CGAUGCCGAC ACCUCUGUCA CCAUCACACC CCAGAGAAC 750
 30 CCACAGGAG CGUGGGAGGU CCAGGUCCU GAGGACCCGG UGGUGGCCU 800
 20 AGUGGGCACC GAUGCCACCC UGCGCUGCUC CUUCUCCCCC GAGCCUGGU 850
 30 UCAGCCUGGC ACAGCUAAC CUACUUGGC ACCUGACAGA CACAAACAG 900
 35 CUGGUOCACA GUUUCACCGA AGGCCCCGGAC CAGGGCAGCG CCTUAUGCCAA 1000
 25 CCGCACGGCC CUCUUCCCGG ACCUGGUUGG ACAAGGCAAU GCAUCCUGA 1050
 40 GGCUGCAGCG CGUGCGUGUG CGGGACGGAGG GCAAGCUAC CUGGUUCGUG 1100
 30 AGCAUCCGGG AUUUCGGCAG CGCUGCCGUC AGCCUGGAGG UGGCCGUCC 1150
 30 CUACUCGAAG CCCAGCAUGA CCCUGGAGCC CAACAGGAC CUGGGCCAG 1200
 45 GGGACACGGU GACCAUCACG UGCUCCAGCU ACCGGGGCUA CCCUGAGGU 1250
 35 GAGGUGUUCU GGCAGGAUGG GCAGGGUGUG CCCUGACUG GCAACGUGAC 1300
 50 CACGUUCGCAG AUGGCCAACG AGCAGGGCUU GUUUGAUGUG CACAGCGUCC 1350

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UGCGGGUGGU CGUUGGUGCC AAUGCACCU ACAGCUGCCU GGUGCGCAAC 1400

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CCCCGUGCUGC ACCAGGAUGC GCACGGCUCU GUCACCAUCA CAGGGCAGCC 1450

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UAUGACAUUC CCCCCAGAGG CCCUGUGGGU GACCGUGGGG CUGUCUGUCU 1500

15

GUUCCAUUGC ACUGCGUGUG CCCUGGGCUU UCGUGUGCUG GAGAAAGAUC 1550

10

AAACAGAGCU GUGAGGAGGA GAAUGCAGGA GCTGAGGACC AGGAUGGGGA 1560

20

GGGAGAAGGC UCCAAGACAG CCCUGCAGCC UCUGAAACAC UCUGACAGCA 1600

15

AAGAAGAUGA UGGACAAGAA AUAGCCUGAC CAUGAGGACC AGGGAGCUGC 1650

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UACCCCUCCC UACAGCUCCU ACCCUCLGGC UCC 1683

which is herein referred to as SEQ ID NO:5.

The ribonucleic acids of the present invention may be prepared using the polynucleotide synthetic methods discussed supra or they may be prepared enzymatically using any one of various RNA polymerases to transcribe a DNA template. This invention also provides nucleic acids, RNA or DNA, which are complementary to SEQ ID NO:1, SEQ ID NO:3, or SEQ ID NO:5.

The present invention also provides probes and primers useful for molecular biology techniques. A compound which encodes for SEQ ID NO:1, SEQ ID NO:3, or SEQ ID NO:5; or a nucleic acid complimentary to SEQ ID NO:1, SEQ ID NO:3, or SEQ ID NO:5; or a fragment thereof and which is at least 18 base pairs in length, and which will selectively hybridize to genomic DNA or messenger RNA encoding a β -secretase protease, is provided. Preferably, the 18 or more base pair compound is DNA.

Primers and probes may be obtained by means well known in the art. For example, once a protein of interest is isolated, restriction enzymes and subsequent gel separation may be used to isolate the fragment of choice.

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The term "selectively hybridize" as used herein may refer to either of two situations. In the first such embodiment of this invention, the nucleic acid compounds described supra hybridize to DNA or RNA encoding a human β -secretase protease under more stringent hybridization conditions

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- 5 than these same nucleic acid compounds would hybridize to nucleic acids encoding analogous β -secretases of another species. In the second such embodiment of this invention, these probes hybridize to the DNA or RNA encoding the β -secretase under more stringent hybridization conditions than other related compounds, including nucleic acid sequences encoding other
- 20 10 amyloid precursor protein proteases.

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These probes and primers can be prepared enzymatically as described supra. In a most preferred embodiment, however, these probes and primers are synthesized using chemical means as described herein.

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- Those skilled in the art will recognize the techniques associated 15 with probes and primers are well known. For example, all or part of the probes or primers may be used to hybridize to the coding sequence. Then, through PCR amplification, the full length sequence may be generated. The full length sequence can be subsequently subcloned into any vector of choice. Alternatively, the primers or probes may be radioactively labeled at the 5' end
- 35 20 in order to screen cDNA libraries by conventional means. A primer or probe can be labeled with a radioactive element which provides for an adequate signal as a means for detection and has sufficient half-life to be useful for detection, such as ^{32}P , 3H , ^{14}C or the like. Other materials which can be used to label the primer or probe include antigens that are recognized by a
- 40 25 specific labeled antibody, fluorescent compounds, enzymes, antibodies specific for a labeled antigen, and chemiluminescent compounds. An appropriate label can be selected having regard to the rate of hybridization and binding of the primer or probe to the nucleotide to be detected and the amount of nucleotide available for hybridization.

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- 50 30 As discussed supra, recombinant DNA cloning vectors and

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expression vectors comprising the nucleic acids of the present invention can be prepared. Many such vectors are illustrated and described above. The preferred nucleic acid vectors are those which are DNA. The preferred recombinant DNA vectors comprise the isolated DNA sequences as given by SEQ ID NO:1 or SEQ ID NO:3. The most preferred recombinant DNA vectors comprise the DNA sequence given by SEQ ID NO:3.

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The skilled artisan understands that the type of cloning vector employed depends upon the availability of appropriate restriction sites, the type of host cell in which the vector is to be transfected or transformed, the purpose of the transfection or transformation (e.g., transient expression in an oocyte system, stable transformation as an extrachromosomal element, or integration into the host chromosome), the presence or absence of readily assayable markers (e.g., antibiotic resistance markers, metabolic markers, or the like), and the number of copies of the gene to be present in the cell.

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30

The type of vector employed to carry the nucleic acids of the present invention may be RNA viruses, DNA viruses, lytic bacteriophages, lysogenic bacteriophages, stable bacteriophages, plasmids, viroids, and the like. When preparing an expression vector, the skilled artisan understands that there are many variables to be considered. One such example is the use of a constitutive promoter, i.e. a promoter which is functional at all times, instead of a regulatable promoter which may be activated or inactivated by the artisan using heat, addition or removal of a nutrient, addition of an antibiotic, and the like. The practitioner also understands that the amount of the nucleic acid or protein to be produced dictates, in part, the selection of the expression system. For experiments examining the amount of the protein expressed on the cell membrane or for experiments examining the biological function of an expressed membrane protein, for example, it may be unwise to employ an expression system which produces too much of the protein. The addition or subtraction of certain sequences, such as a signal sequence preceding the coding sequence, may be employed by the practitioner to

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influence localization of the resulting polypeptide. Such sequences added to or removed from the nucleic acid compounds of the present invention are encompassed within this invention.

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Plasmids can be readily modified to construct expression vectors 5 in a variety of organisms, including, but not limited to, E. coli, SF9 (as host for baculovirus), Spodoptera and Saccharomyces. See: Serok et al., Molecular Cloning: A Laboratory Manual (1989)

20

One of the most widely employed techniques for altering a nucleic acid sequence is by way of oligonucleotide-directed site-specific 10 mutagenesis. B Comack, "Current Protocols in Molecular Biology", 8.01-8.5.9, (F. Ausubel, et al., eds. 1991). In this technique an oligonucleotide, whose sequence contains the mutation of interest, is synthesized as described supra. This oligonucleotide is then hybridized to a template containing the wild-type 25 sequence. In a most preferred embodiment of this technique, the template is 15 a single-stranded template. Particularly useful are plasmids which contain regions such as the f1 intergenic region. This region allows the generation of 30 single-stranded templates when a helper phage is added to the culture harboring the "phagemid".

35

After the annealing of the oligonucleotide, to the template, a 20 DNA-dependent DNA polymerase is then used to synthesize the second strand from the oligonucleotide, complementary to the template DNA. The resulting product is a heteroduplex molecule containing a mismatch due to 40 the mutation in the oligonucleotide. After DNA replication by the host cell a mixture of two types of plasmid are present, the wild-type and the newly 45 constructed mutant. This technique permits the introduction of convenient restriction sites such that the coding sequence may be placed immediately adjacent to whichever transcriptional or translational regulatory elements are employed by the practitioner.

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The construction protocols utilized for E. coli can be followed to 30 construct analogous vectors for other organisms, merely by substituting, if

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necessary, the appropriate regulatory elements using techniques well known to skilled artisans.

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Host cells which harbor the nucleic acids provided by the present invention can also be prepared. One suitable host cell is an

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5 Xenopus sp. oocyte which has been injected with RNA or DNA compounds of the present invention. Preferred oocytes of the present invention are those which harbor a sense mRNA of the present invention. Other preferred host cells include HeLa and 293 cells which have been transfected and/or transformed with a vector which comprises a nucleic acid of the present

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invention.

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A method for constructing a recombinant host cell capable of expressing SEQ ID NO:2 or SEQ ID NO:4 is also possible with regard to the present invention, said method comprising transforming a host cell with a recombinant DNA vector that comprises an isolated DNA sequence which

15 encodes SEQ ID NO:2 or SEQ ID NO:4. The preferred host cell is 293 cells.

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A preferred vector for expression is one which comprises SEQ ID NO:1 or SEQ ID NO:3, most preferably SEQ ID NO:1. Transformed host cells may be cultured under conditions well known to skilled artisans such that SEQ ID NO: 2 or SEQ ID NO:4 are expressed, thereby producing the sequence of β -

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20 secretase in the recombinant host cell.

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A further embodiment of the invention consists of a method of isolating and purifying an amyloid precursor protein protease from a host cell expressing said protein. In this embodiment, a host cell, either prokaryotic or eukaryotic, expressing amyloid precursor protein protease, is cultured in an appropriate medium until a substantial cell mass has been obtained. The second step of this embodiment is the isolation of amyloid precursor protein protease from the cultured cells. Two methods for purifying amyloid precursor protein protease from a non-transformed mammalian cell line are described in United States Patent Number 5,328,842, the entire contents of

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which are herein incorporated by reference. The following summarizes those methods.

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Once grown and harvested, the cultured cells are lysed by nitrogen cavitation in the presence of protease inhibitors. A soluble fraction 5 is prepared from the lysate by ultracentrifugation. The resulting solution of cytosolic proteins contains β -secretase and is subjected to a series of 15 purification procedures.

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The soluble fraction of the cell lysate is run through a series of 20 column chromatography procedures. Anion exchange chromatography is followed by hydrophobic interaction, molecular sizing, and finally another 10 hydrophobic interaction technique where the conditions are such that the β -secretase binds the resin weakly. Each column is run individually, and the eluate is collected in fractions while monitoring for absorbance at 280 nm. 25 Fractions are assayed for β -secretase activity, and those fractions with the desired activity are then run over the next column until a homogeneous 15 solution of β -secretase is obtained.

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Immunoaffinity purification using anti- β -secretase antibodies is 35 an alternative to the series of chromatographic procedures already mentioned. Making antiserum or monoclonal antibodies directed against a purified protein is well known in the art, and skilled artisans readily will be 20 able to prepare anti- β -secretase antibodies. Preparing an immunoaffinity matrix using such antibodies and isolating β -secretase using the immunoaffinity matrix is also well within the skill of the art. See, AFFINITY CHROMATOGRAPHY PRINCIPLES & METHODS, Pharmacia Fine Chemicals, 1983.

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45 The ability of an agent to inhibit the protein of the present invention is essential in the development of a multitude of indications. In developing agents which act as inhibitors of β -secretase, it would be desirable, therefore, to determine those agents which interact with the protein of the present invention. Generally, such an assay includes a method for 50 determining whether a substance is a functional ligand of β -secretase, said

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method comprising contacting a functional compound of the β -secretase with said substance, monitoring enzymatic activity by physically detectable means, and identifying those substances which effect a chosen response.

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The instant invention provides such a screening system useful for discovering agents which inhibit the β -secretase, said screening system comprising the steps of:

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- a) isolating a β -secretase;
- b) exposing said β -secretase to a potential inhibitor of the β -secretase;
- c) introducing a suitable substrate;
- d) quantifying the amount of cleavage of the substrate relative to a control in which no potential inhibitor has been introduced.

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This allows one to rapidly screen for inhibitors of β -secretase.

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Utilization of the screening system described above provides a sensitive and rapid means to determine compounds which inhibit β -secretase. This screening system may also be adapted to automated procedures such as a PANDEX® (Baxter-Dade Diagnostics) system allowing for efficient high-volume screening of potential therapeutic agents. In such a screening protocol a protein protease is prepared as elsewhere described herein, preferably using recombinant DNA technology. A sample of a test compound is then introduced to the reaction vessel containing the protein protease followed by the addition of an appropriate substrate. In the alternative the substrate may be added simultaneously with the test compound.

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25 The desirability of a bioactivity assay system which determines the response of β -secretase to a compound of interest is clear. The instant invention provides such a bioactivity assay, said assay comprising the steps of:

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a) transfecting a mammalian host cell with an expression vector comprising DNA encoding β -secretase;

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b) culturing said host cell under conditions such that the β -secretase protein is expressed;

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c) exposing said host cell so transfected to a test compound; and
d) measuring the change in a physiological condition known to be influenced by β -secretase relative to a control in which the transfected host cell is not exposed to a test compound.

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The present invention comprises a method of using said

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inhibitors of β -secretase in the treatment of patients with acquired disease states of the brain including Alzheimer's disease. As used herein, "patient" refers to a mammal such a rat, mouse, guinea pig, dog, or human. It is understood, however, that the preferred patient for use with the methods herein is a human patient. As used herein, the term "treatment" (or "treat")

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or "treating") includes its generally accepted meaning which encompasses prohibiting, preventing, restraining, and slowing, stopping, or reversing the progression, severity, and resulting symptoms of acquired disease states of the brain. As such, the methods of the present invention encompass both therapeutic and prophylactic uses.

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Compounds which are inhibitors of β -secretase are usually administered in the form of pharmaceutical compositions. These compounds can be administered by a variety of routes including oral, rectal, transdermal, subcutaneous, intravenous, intramuscular, and intranasal. These compounds are effective as both injectable and oral compositions. Such compositions are

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prepared in a manner well known in the pharmaceutical art and comprise at least one active compound.

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The present invention also includes methods employing pharmaceutical compositions which contain, as the active ingredient,

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5 inhibitors of β -secretase associated with pharmaceutically acceptable carriers.

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In making the compositions of the present invention the active ingredient is usually mixed with an excipient, diluted by an excipient or enclosed within such a carrier which can be in the form of a capsule, sachet, paper or other container. When the excipient serves as a diluent, it can be a solid, semi-

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10 solid, or liquid material, which acts as a vehicle, carrier or medium for the active ingredient. Thus, the compositions can be in the form of tablets, pills, powders, lozenges, sachets, cachets, elixirs, suspensions, emulsions, solutions, 15 syrups, aerosols (as a solid or in a liquid medium), ointments containing for example up to 10% by weight of the active compound, soft and hard gelatin capsules, suppositories, sterile injectable solutions, and sterile packaged powders.

30

In preparing a formulation, it may be necessary to mill the active compound to provide the appropriate particle size prior to combining with the other ingredients. If the active compound is substantially insoluble,

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20 it ordinarily is milled to a particle size of less than 200 mesh. If the active compound is substantially water soluble, the particle size is normally adjusted by milling to provide a substantially uniform distribution in the formulation, e.g. about 40 mesh.

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Some examples of suitable excipients include lactose, dextrose, 25 sucrose, sorbitol, mannitol, starches, gum acacia, calcium phosphate, 45 alginates, tragacanth, gelatin, calcium silicate, microcrystalline cellulose, polyvinylpyrrolidone, cellulose, water, syrup, and methyl cellulose. The formulations can additionally include: lubricating agents such as talc, magnesium stearate, and mineral oil; wetting agents; emulsifying and 50 suspending agents; preserving agents such as methyl- and

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propylhydroxybenzoates; sweetening agents; and flavoring agents. The compositions of the invention can be formulated so as to provide quick, sustained or delayed release of the active ingredient after administration to the patient by employing procedures known in the art.

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5 The compositions are preferably formulated in a unit dosage form, each dosage containing from about 5 to about 100 mg, more usually about 10 to about 30 mg, of the active ingredient. The term "unit dosage form" refers to physically discrete units suitable as unitary dosages for human subjects and other mammals, each unit containing a predetermined quantity of active material calculated to produce the desired therapeutic effect, in association with a suitable pharmaceutical excipient.

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10 The active compound is effective over a wide dosage range. For examples, dosages per day normally fall within the range of about 0.5 to about 30 mg/kg of body weight. In the treatment of adult humans, the range 15 of about 1 to about 15 mg/kg/day, in single or divided dose, is especially preferred. However, it will be understood that the amount of the compound actually administered will be determined by a physician, in the light of the relevant circumstances, including the condition to be treated, the chosen route of administration, the actual compound administered, the age, weight, 20 and response of the individual patient, and the severity of the patient's symptoms, and therefore the above dosage ranges are not intended to limit the scope of the invention in any way. In some instances dosage levels below the lower limit of the aforesaid range may be more than adequate, while in other cases still larger doses may be employed without causing any harmful 25 side effect, provided that such larger doses are first divided into several smaller doses for administration throughout the day.

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40 For preparing solid compositions such as tablets the principal active ingredient is mixed with a pharmaceutical excipient to form a solid preformulation composition containing a homogeneous mixture of a 45 30 compound of the present invention. When referring to these preformulation

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compositions as homogeneous, it is meant that the active ingredient is dispersed evenly throughout the composition so that the composition may be readily subdivided into equally effective unit dosage forms such as tablets, pills and capsules. This solid preformulation is then subdivided into unit dosage forms of the type described above containing from 0.1 to about 500 mg of the active ingredient of the present invention.

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The tablets or pills of the present invention may be coated or otherwise compounded to provide a dosage form affording the advantage of prolonged action. For example, the tablet or pill can comprise an inner dosage and an outer dosage component, the latter being in the form of an envelope over the former. The two components can be separated by enteric layer which serves to resist disintegration in the stomach and permit the inner component to pass intact into the duodenum or to be delayed in release. A variety of materials can be used for such enteric layers or coatings, such materials including a number of polymeric acids and mixtures of polymeric acids with such materials as shellac, cetyl alcohol, and cellulose acetate.

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The liquid forms in which the novel compositions of the present invention may be incorporated for administration orally or by injection include aqueous solutions, suitably flavored syrups, aqueous or oil suspensions, and flavored emulsions with edible oils such as cottonseed oil, sesame oil, coconut oil, or peanut oil, as well as elixirs and similar pharmaceutical vehicles.

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Compositions for inhalation or insufflation include solutions and suspensions in pharmaceutically acceptable, aqueous or organic solvents, or mixtures thereof, and powders. The liquid or solid compositions may contain suitable pharmaceutically acceptable excipients as described supra. Preferably the compositions are administered by the oral or nasal respiratory route for local or systemic effect. Compositions in preferably pharmaceutically acceptable solvents may be nebulized by use of inert gases. Nebulized solutions may be breathed directly from the nebulizing device or

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the nebulizing device may be attached to a face mask, tent, or intermittent positive pressure breathing machine. Solution, suspension, or powder compositions may be administered, preferably orally or nasally, from devices which deliver the formulation in an appropriate manner.

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5 The following examples illustrate the pharmaceutical compositions of the present invention.

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Formulation Preparation 1

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Hard gelatin capsules containing the following ingredients are prepared:

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	<u>Ingredient</u>	Quantity (mg/capsule)
	Active Ingredient	30.0

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10	Starch	305.0
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	Magnesium stearate	5.0
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The above ingredients are mixed and filled into hard gelatin capsules in 340 mg quantities.

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Formulation Preparation 2

A tablet formula is prepared using the ingredients below:

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	<u>Ingredient</u>	Quantity (mg/tablet)
	Active Ingredient	25.0

25	Cellulose, microcrystalline	200.0
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	Colloidal silicon dioxide	10.0
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Stearic acid 5.0

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The components are blended and compressed to form tablets,
each weighing 240 mg.

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Formulation Preparation 3

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A dry powder inhaler formulation is prepared containing the
following components:

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	<u>Ingredient</u>	<u>Weight %</u>
10	Active Ingredient	5
	Lactose	95

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The active mixture is mixed with the lactose and the mixture is
added to a dry powder inhaling appliance.

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Formulation Preparation 4

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Tablets, each containing 30 mg of active ingredient, are prepared
20 as follows:

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	<u>Ingredient</u>	<u>Quantity</u> (mg/tablet)
20	Active Ingredient	30.0 mg
25	Starch	45.0 mg
	Microcrystalline cellulose	35.0 mg
	Polyvinylpyrrolidone	
30	(as 10% solution in water)	4.0 mg

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Sodium carboxymethyl starch	4.5 mg
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Magnesium stearate	0.5 mg
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Talc	<u>1.0 mg</u>
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Total	120 mg
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10 The active ingredient, starch and cellulose are passed through a No. 20 mesh U.S. sieve and mixed thoroughly. The solution of polyvinylpyrrolidone is mixed with the resultant powders, which are then passed through a 16 mesh U.S. sieve. The granules so produced are dried at 50-60°C and passed through a 16 mesh U.S. sieve. The sodium carboxymethyl starch, magnesium stearate, and talc, previously passed through a No. 30 mesh U.S. sieve, are then added to the granules which, after mixing, are compressed on a tablet machine to yield tablets each weighing 120 mg.

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15 carboxymethyl starch, magnesium stearate, and talc, previously passed through a No. 30 mesh U.S. sieve, are then added to the granules which, after mixing, are compressed on a tablet machine to yield tablets each weighing 120 mg.

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20 Formulation Preparation 5

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Capsules, each containing 40 mg of medicament are made as

follows:

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25	Quantity
	<u>(mg/capsule)</u>
Active Ingredient	40.0 mg
Starch	109.0 mg

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Magnesium stearate	<u>1.0 mg</u>
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Total	150.0 mg
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5 The active ingredient, cellulose, starch, and magnesium stearate
 15 are blended, passed through a No. 20 mesh U.S. sieve, and filled into hard
 gelatin capsules in 150 mg quantities.

Formulation Preparation 6

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Suppositories, each containing 25 mg of active ingredient are
 made as follows:

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	<u>Ingredient</u>	<u>Amount</u>
15	Active Ingredient	25 mg
30	Saturated fatty acid glycerides to	2,000 mg

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20 The active ingredient is passed through a No. 60 mesh U.S. sieve
 20 and suspended in the saturated fatty acid glycerides previously melted using
 the minimum heat necessary. The mixture is then poured into a suppository
 mold of nominal 2.0 g capacity and allowed to cool.

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Formulation Preparation 7

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Suspensions, each containing 50 mg of medicament per 5.0 ml
 dose are made as follows:

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	<u>Ingredient</u>	<u>Amount</u>
30	Active Ingredient	50.0 mg

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Xanthan gum **4.0 mg**

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Sodium carboxymethyl cellulose (11%)

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5 **Microcrystalline cellulose (89%)** **50.0 mg**

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Sucrose **1.75 g**

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Sodium benzoate **10.0 mg**

35

Flavor and Color **q.v.**

40

Purified water to **5.0 ml**

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15 The medicament, sucrose and xanthan gum are blended, passed through a No. 10 mesh U.S. sieve, and then mixed with a previously made
30 solution of the microcrystalline cellulose and sodium carboxymethyl cellulose in water. The sodium benzoate, flavor, and color are diluted with some of the
35 water and added with stirring. Sufficient water is then added to produce the
20 required volume.

Formulation Preparation 8

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40 Capsules, each containing 15 mg of medicament, are made as
25 follows:

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45	Quantity
	(mg/capsule)
Ingredient	
Active Ingredient	15.0 mg

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	Starch	407.0 mg
10	Magnesium stearate	<u>3.0 mg</u>
15	5 Total	425.0 mg

15 The active ingredient, cellulose, starch, and magnesium stearate
are blended, passed through a No. 20 mesh U.S. sieve, and filled into hard
gelatin capsules in 425 mg quantities.

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Formulation Preparation 9

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An intravenous formulation may be prepared as follows:

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	<u>Ingredient</u>	<u>Quantity</u>
30	Active Ingredient	250.0 mg
35	Isotonic saline	1000 ml

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Formulation Preparation 10

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A topical formulation may be prepared as follows:

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	<u>Ingredient</u>	<u>Quantity</u>
45	Active Ingredient	1-10 g
50	Emulsifying Wax	30 g
55	Liquid Paraffin	20 g

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- White Soft Paraffin** to 100 g
- The white soft paraffin is heated until molten. The liquid paraffin and emulsifying wax are incorporated and stirred until dissolved. The active ingredient is added and stirring is continued until dispersed. The mixture is then cooled until solid.

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Formulation Preparation 11

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Sublingual or buccal tablets, each containing 10 mg of active ingredient, may be prepared as follows:

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	<u>Quantity</u>
	<u>Per Tablet</u>
15 <u>Ingredient</u>	
Active Ingredient(s)	10.0 mg
30 Glycerol	210.5 mg
20 Water	143.0 mg
35 Sodium Citrate	4.5 mg
40 Polyvinyl Alcohol	26.5 mg
25 Polyvinylpyrrolidone	15.5 mg
45 Total	410.0 mg

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The glycerol, water, sodium citrate, polyvinyl alcohol, and polyvinylpyrrolidone are admixed together by continuous stirring and

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maintaining the temperature at about 90°C. When the polymers have gone into solution, the solution is cooled to about 50-55°C and the medicament is slowly admixed. The homogenous mixture is poured into forms made of an inert material to produce a drug-containing diffusion matrix having a thickness of about 2-4 mm. This diffusion matrix is then cut to form individual tablets having the appropriate size.

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Another preferred formulation employed in the methods of the present invention employs transdermal delivery devices ("patches"). Such transdermal patches may be used to provide continuous or discontinuous infusion of the compounds of the present invention in controlled amounts. The construction and use of transdermal patches for the delivery of pharmaceutical agents is well known in the art. See, e.g., U.S. Patent 5,023,252, issued June 11, 1991, herein incorporated by reference. Such patches may be constructed for continuous, pulsatile, or on demand delivery of pharmaceutical agents.

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Frequently, it will be desirable or necessary to introduce the pharmaceutical composition to the brain, either directly or indirectly. Direct techniques usually involve placement of a drug delivery catheter into the host's ventricular system to bypass the blood-brain barrier. One such implantable delivery system, used for the transport of biological factors to specific anatomical regions of the body, is described in U.S. Patent 5,011,472, issued April 30, 1991, which is herein incorporated by reference.

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Indirect techniques, which are generally preferred, usually involve formulating the compositions to provide for drug latentiation by the conversion of hydrophilic drugs into lipid-soluble drugs or prodrugs. Latentiation is generally achieved through blocking of the hydroxy, carbonyl, sulfate, and primary amine groups present on the drug to render the drug more lipid soluble and amenable to transportation across the blood-brain barrier. Alternatively, the delivery of hydrophilic drugs may be enhanced by

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intra-arterial infusion of hypertonic solutions which can transiently open the blood-brain barrier.

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The proteins of this invention as well as fragments of these proteins may be used as antigens for the synthesis of antibodies. The term

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5 "antibody" as used herein describes antibodies, fragments of antibodies (such as, but not limited, to Fab, Fab', Fab₂', and Fv fragments), and chimeric, humanized, veneered, resurfaced, or CDR-grafted antibodies capable of binding antigens of a similar nature as the parent antibody molecule from which they are derived. The instant invention also encompasses single chain

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10 polypeptide binding molecules.

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The term "antibody" as used herein is not limited by the manner in which the antibodies are produced, whether such production is in situ or not. The term "antibody" as used in this specification encompasses those antibodies produced by recombinant DNA technology means including, but 15 not limited, to expression in bacteria, yeast, insect cell lines, or mammalian cell lines.

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The production of antibodies, both monoclonal and polyclonal, in animals, especially mice, is well known in the art. See, e.g., C. Milstein,

HANDBOOK OF EXPERIMENTAL IMMUNOLOGY, (Blackwell Scientific Pub., 1986);

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20 J. Goding, MONOCLONAL ANTIBODIES: PRINCIPLES AND PRACTICE, (Academic Press, 1983). For the production of monoclonal antibodies the basic process begins with injecting a mouse, or other suitable animal, with an immunogen. The mouse is subsequently sacrificed and cells taken from its spleen are fused 40 with myeloma cells, resulting in a hybridoma that reproduces in vitro. The 25 population of hybridomas is screened to isolate individual clones, each of which secretes a single antibody species, specific for the immunogen. The individual antibody species obtained in this way is each the product of a single B cell from the immune animal generated in response to a specific antigenic site, or epitope, recognized on the immunogenic substance.

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Chimeric antibodies are described in U.S. Patent No. 4,816,567, which issued March 28, 1989 to S. Cabilly, *et al.* This reference discloses methods and vectors for the preparation of chimeric antibodies. The entire contents of U.S. Patent No. 4,816,567 are herein incorporated by reference.

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5 An alternative approach to production of genetically engineered antibodies is provided in U.S. Patent No. 4,816,397, which also issued March 28, 1989 to M. Boss, *et al.*, the entire contents of which are herein incorporated by reference. The Boss patent teaches the simultaneous co-expression of the heavy and light chains of the antibody in the same host cell.

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10 The approach of U.S. Patent 4,816,397 has been further refined as taught in European Patent Publication No. 0 239 400, which published September 30, 1987. The teachings of this European patent publication (Winter) are a preferred format for the genetic engineering of the reactive monoclonal antibodies of this invention. The Winter technology involves the 15 replacement of complementarity determining regions (CDRs) of a human antibody with the CDRs of a murine monoclonal antibody thereby converting the specificity of the human antibody to the specificity of the murine antibody which was the source of the CDR regions. This "CDR grafting" technology affords a molecule containing minimal murine sequence and thus is less 20 immunogenic.

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Single chain antibody technology is yet another variety of genetically engineered antibody which is now well known in the art. See, e.g., R.E. Bird, *et al.*, Science 242:423-426 (1988); PCT Publication No. WO 40 88/01649, which was published 10 March 1988; United States Patent 25 5,260,203, issued November 9, 1993, the entire contents of which are herein incorporated by reference. The single chain antibody technology involves 45 joining the binding regions of heavy and light chains with a polypeptide sequence to generate a single polypeptide having the binding specificity of the antibody from which it was derived.

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The aforementioned genetic engineering approaches provide the skilled artisan with numerous means to generate molecules which retain the binding characteristics of the parental antibody while affording a less immunogenic format.

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5 These antibodies are used in diagnostics, therapeutics or in diagnostic/therapeutic combinations. By "diagnostics" as used herein is meant testing that is related to either the in vitro or in vivo diagnosis of disease states or biological status in mammals, preferably in humans. By "therapeutics" and "therapeutic/diagnostic combinations" as used herein is 10 respectively meant the treatment or the diagnosis and treatment of disease states or biological status by the in vivo administration to mammals, preferably humans, of the antibodies of the present invention. The antibodies 15 of the present invention are especially preferred in the diagnosis and/or treatment of conditions associated with an excess or deficiency of β -secretase.

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Claims

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5 WHAT IS CLAIMED IS:

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1. An isolated amino acid compound functional as an amyloid precursor protein protease which comprises the amino acid sequence given by SEQ ID NO:2 or SEQ ID NO:4, or a functional equivalent thereof, or a fragment of at least 6 continuous amino acids thereof.

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2. A nucleic acid compound encoding the amino acid compound of Claim 1.

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3. A nucleic acid compound encoding the amino acid compound of Claim 1 which comprises the nucleic acid sequence given by SEQ ID NO:1 or SEQ ID NO:3.

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4. A composition comprising an isolated nucleic acid compound containing a sequence encoding an amyloid precursor protein protease as claimed in Claim 2, wherein said sequence is selected from the group consisting of

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(a) SEQ ID NO:1 or SEQ ID NO:3;

(b) nucleotides 25 through 1629 of SEQ ID NO:1 or SEQ ID NO:3;

(c) SEQ ID NO:5;

(d) nucleotides 25 through 1629 of SEQ ID NO:5;

(e) a nucleic acid complimentary to (a), (b), (c), or (d); and

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- (i) a fragment of (a), (b), (c), (d), or (e) that is at least 18 bases in length and which will selectively hybridize to human genomic DNA encoding an amyloid precursor protein protease.

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5. The composition as claimed in Claim 4 wherein the isolated nucleic acid is deoxyribonucleic acid.

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6. The composition as claimed in Claim 5 wherein the deoxyribonucleic acid is SEQ ID NO:1 or SEQ ID NO:3, or a sequence complimentary to SEQ ID NO:1 or SEQ ID NO:3.

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7. The composition of Claim 5 wherein the deoxyribonucleic acid is nucleotides 25 through 1629 of SEQ ID NO:1 or SEQ ID NO:3, or a sequence complimentary to nucleotides 25 through 1629 of SEQ ID NO:1.

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8. The composition as claimed in Claim 4 wherein the isolated nucleic acid is ribonucleic acid.

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9. The composition as claimed in Claim 8 wherein the ribonucleic acid is SEQ ID NO:5 or a sequence complimentary to SEQ ID NO:5.

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10. The composition of Claim 8 wherein the ribonucleic acid is nucleotides 25 through 1629 of SEQ ID NO:5 or a sequence complimentary to nucleotides 25 through 1629 of SEQ ID NO:5.

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11. An expression vector capable of producing an amyloid precursor protein protease in a host cell which comprises a nucleic acid

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compound as claimed in Claim 4 in combination with regulatory elements necessary for expression of the nucleic acid compound in a host cell.

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12. An expression vector as claimed in Claim 11 for use in a host cell wherein said host cell is a mammalian cell.

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13. An expression vector as claimed in Claim 11 for use in a host cell wherein said host cell is a prokaryotic cell.

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14. A transfected host cell harboring an expression vector as claimed in Claim 11.

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15. A transfected host cell as claimed in Claim 14 wherein the host cell is a mammalian cell.

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16. A transfected host cell as claimed in Claim 14 wherein the host cell is a prokaryotic cell.

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17. A method to identify compounds which inhibit the synthesis or release of beta-amyloid protein, which method comprises:

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(a) isolating a β -secretase;

(b) exposing said β -secretase to a potential inhibitor of the β -secretase;

(c) introducing a suitable substrate;

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(d) quantifying the amount of cleavage of the substrate relative to a control in which no potential inhibitor has been introduced.

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18. The method of Claim 17 wherein said β -secretase comprises the amino acid sequence given by SEQ ID NO:2 or SEQ ID NO:4.

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10 19. A method of evaluating the effectiveness of a test compound
for the treatment or prevention of a condition associated with the synthesis or
release of beta-amyloid protein, which method comprises:

- 15 (a) transfecting a mammalian host cell with an expression
vector comprising DNA encoding β -secretase;
15 (b) culturing said host cell under conditions such that the β -
secretase protein is expressed;
20 (c) exposing said host cell so transfected to a test compound;
and
20 (d) measuring the change in a physiological condition known to
be influenced by β -secretase relative to a control in which the
transfected host cell is not exposed to a test compound.

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25 20. The method of Claim 19 wherein said β -secretase comprises
the amino acid sequence given by SEQ ID NO:2 or SEQ ID NO:4.

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30 21. A method of treating or preventing Alzheimer's Disease or
other neurodegenerative disorders in a patient which comprises
administering to a patient in need thereof, an effective amount of an inhibitor
of the amyloid precursor protein protease given by the amino acid sequence of
35 SEQ ID NO:2 or SEQ ID NO:4.

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20 22. A pharmaceutical composition comprising an inhibitor of the
amyloid precursor protein protease given by SEQ ID NO:2 or SEQ ID NO:4,
in combination with one or more pharmaceutically acceptable excipients,
carriers, or diluents therefor.

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INTERNATIONAL SEARCH REPORT

International Application No.
PCT/US 00/06707

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C07K14/47 C12N15/57 C12N9/64 C12N5/10 C12N5/16
A61P25/28

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C12N C07K A61P

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

STRAND, EMBL, GENSEQ, EPO-Internal

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE GENEMBL 'Online! 6 June 1996 (1996-06-06) HILLIER ET AL.: "yx480g8.rl soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:265022 5' similar to contains Alu repetitive element" XP002148339 Accession number N30496	1-16
X	WO 96 40885 A (MCCONLOGUE LISA C ;KEIM PAMELA S (US); SINHA SUKANTO (US); TAK HUA) 19 December 1996 (1996-12-19) Page 22, line 20 -page 23, line 2 Page 41, line 20 -page 48, line 34 claims 23-41; table 3	17 -/-

Further documents are listed in the continuation of box C.

Patent family members are listed in annex.

* Special categories of cited documents:

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the International filing date
- *L* document which may throw doubt on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (not specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the International filing date but later than the priority date claimed

- *T* later document published after the International filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
- *Z* document member of the same patent family

Date of the actual completion of the international search 4 October 2000	Date of mailing of the International search report 17/10/2000
Name and mailing address of the ISA European Patent Office, P.B. 3010 Patentlaan 2 NL - 2200 HV Rijswijk Tel. (+31-70) 340-2040, Te. 31 651 epo nl, Fax (+31-70) 340-3016	Authorized officer ALCONADA RODRIG... A

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 00/06707

C. (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Description of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EP 0 653 154 A (HOECHST JAPAN) 17 May 1995 (1995-05-17) page 5, line 13-21 claim 10	19
A	DATABASE SWISSPROT 'Online' 1 June 1998 (1998-06-01) HUSAINI ET AL.: "Bos taurus butyrophilin fragment" XP002148340 Accession No. 046535	1-16
P,X	WO 99 46281 A (BAKER KEVIN P ;CHEN JIAN (US); GENENTECH INC (US); GURNEY AUSTIN () 16 September 1999 (1999-09-16) page 12, line 24-35 page 60, line 10-29 page 128, line 15-22 page 149, line 30-33 page 151, line 22-30 page 159, line 17-19	1-16

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 21,22

Claims 21 and 22 refer to an antagonist/inhibitor of the polypeptide without giving a true technical characterization. Moreover, no such compounds are defined in the application. In consequence, the scope of said claims is ambiguous and vague, and their subject-matter is not sufficiently disclosed and supported (Art. 6 PCT). No search could be carried out for such purely speculative claims whose wording is, in fact, a mere recitation of the result to be achieved.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No	
PCT/US 00/06707	

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